

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

5 BERGERON, Michel G. ¹, 1145 des Érables, Québec City,
 Québec, Canada, G2K 1T8
 BOISSINOT, Maurice ¹, 109 Jean-Bruchési, St-Augustin-
 de-Desmaures, Québec, Canada, G3A 2N2
 10 HULETSKY, Ann ¹, 1231 Av des Pins, Sillery, Québec,
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 ROY, Paul H. ², 28 Charles Garnier, Loretteville,
 Québec, Canada, G2A 2X8

20 ¹:Canadian citizenship
²:American citizenship

(ii) TITLE OF THE INVENTION: HIGHLY CONSERVED GENES AN THEIR
 USE TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC AND
 25 UNIVERSAL NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO
 RAPIDLY DETECT AND IDENTIFY ALGAL, ARCHAEAL, BACTERIAL,
 FUNGAL AND PARASITICAL MICROORGANISMS FROM CLINICAL
 SPECIMENS FOR DIAGNOSIS

30 (iii) NUMBER OF SEQUENCES: 2297

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE:
 35 (B) STREET:
 (C) CITY:
 (D) STATE:
 (E) COUNTRY:
 (F) ZIP:

40 (v) COMPUTER READABLE:

(A) MEDIUM TYPE:
 (B) COMPUTER:
 45 (C) OPERATING:
 (D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

50 (A) APPLICATION:
 (B) FILING DATE:
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

55 (A) APPLICATION:
 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME:
- (B) REGISTRATION NUMBER:

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(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE:
- (B) TELEFAX:

2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
 (B) STRAIN: ATCC 19606

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

	CAAACTCGTG	AGCACATCCT	TCTTTCTCGT	CAGGTAGGTG	TACCTTACAT	50
	CATCGTATTC	TTAAACAAAT	GCGACCTTGT	TGATGACGAA	GAATTACTTG	100
20	AATTAGTAGA	AATGGAAGTA	CGTGAACCTC	TTTCTACTTA	TGACTTCCCA	150
	GGTGATGACA	CTCCAGTAAT	CCGTGGTTCA	GCTCTTGCA	CGCTTAACGG	200
	TGAAGCTGGT	CCTTACGGTG	AAGAATCAGT	TCTTGCTCTT	GTAGCAGCAC	250
	TTGACTCTTA	CATCCCAGAG	CCAGAGCGTG	CAATCGACAA	AGCATTCCTG	300
	ATGCCAATCG	AAGACGTATT	CTCAATTTCT	GGTCGTGGTA	CAGTAGTAAC	350
25	AGGCCGTGTT	GAAGCTGGTA	TCATCAAAGT	TGGTGAAGAA	GTAGAGATCG	400
	TTGGTATTAA	AGATACAGTT	AAAACAACTG	TAACTGGCGT	AGAAATGTTC	450
	CGTAAACTTC	TTGACGAAGG	CCGTGCAGGT	GAGAACTGTG	GTATCTTACT	500
	TCGTGGTACT	AAGCGTGAAG	AAGTACAACG	TGGTCAAGTA	CTTGCTAAAC	550
	CAGGTACAAT	CAAGCCGCAC	ACTAAATTCG	ACGCAGAAGT	ATACGTACTT	600
30	TCTAAAGAAG	AAGGTGGTCG	TCACACTCCA	TTCTTAAATG	GTTACCGTCC	650
	ACAGTTCTAC	TTCCGTACAA	CTGACGTAAC	TGGTGCRATC	CAGTTGAAAG	700
	AAGGCGTTGA	AATGGTAATG	CCAGGTGACA	ACGTTGAAAT	GTCAGTAGAA	750

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2) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
 (B) STRAIN: ATCC 35568

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

	CGGTGCGATC	CTCGTGCTCG	CCGCGACCGA	CGGCCCATG	GCCCAGACCC	50
	GCGAGCACGT	CCTGCTCGCC	CGTCAGGTCG	GCGTTCCAC	CATCCTCATC	100
	GCCCTCAACA	AGTCCGACAT	GGTTGACGAC	GAGGAAATGA	TGGAAGTGGT	150
55	CGAGGAGGAG	TGCCGCGACC	TGCTGGAGTC	CCAGGACTTC	GATCGCGATG	200
	CCCCGATCGT	CCAGGTTTCC	GCTCTGAAGG	CCCTCGAGGG	CGACGCGGAG	250
	TGGGTTGCCA	AGATCGAGGA	GCTCATGGAG	GCTGTGGATT	CCTACATCCC	300
	CACCCCGGAG	CGCGATATGG	ACAAGCCCTT	CCTCATGCCG	ATCGAGGACG	350
	TCTTCACGAT	CACAGGTCGT	GGCACGGTCG	TCACGGGGCG	TGTTGAGCGT	400
60	GGCAAGCTGC	CGATCAACTC	CGAGGTCGAG	ATCCTCGGTA	TCCGTGATCC	450

CCAGAAGACC ACGGTCACCG GCATCGAGAT GTTCCACAAG TCGATGGACG 500
 AGGCATGGGC CGGCGAGAAC TGTGGCCTGC TGCTGCGCGG TACCAAGCGC 550
 GATGAGGTTG AGCGCGGCCA GGTTGTGGCC ATTCCCGGCT CCATCACGCC 600
 TCACACCGAG TTCGAGGGCC AGGTTTACAT CCTCAAGAAG GAAGAGGGCG 650
 5 GCCGTCACAA CCCGTTCTTC TCGAACTACC GTCCGCAGTT CTACTTCCGT 700
 ACCACGGACG TGACCGGCGT CATCACCCCTC CCCGAGGGCA CCGACATGGT 750
 CATGCCTGGC GACACCACCG AGATCTCCGT TCAGCTGATC CAGCCCATCG 800
 CCATGGAGCC CGGCTGGGCT TCGCCA 826

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2) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aerococcus viridans*
 (B) STRAIN: ATCC 11563

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

TGGTGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAAACTC 50
 GTGAGCACAT CCTTTTAGCT GGCCAAATCG GTGTTCTTGC ATTCGTAGTA 100
 30 TTCTTAAACA AAGTTGACCA AGTTGACGAT GAAGAATTAC TAGAATTAGT 150
 TGAAATGGAA GTTCGTGACT TATTATCTGA GTACAACTAC CCAGGTGACG 200
 ATCTACCTGT AATCGCTGGT TCTGCTTTAT TAGCATTACA AGGCGATGAA 250
 GCTCAAGAAG CTAAATCAT GGAATTAATG GAAGCTGTAG ACTCTTACAT 300
 TCCAGAACCA GAACGTGACA ACGACAAACC ATTCATGATG CCAATTGAGG 350
 35 ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA 400
 CGTGGTGAAG TTCGTACAGG TGACGAAGTT GACATCGTTG GTATTGCTGA 450
 ACAATCGGT AAATCAGTTG TAACTGGTGT TGAAATGTTT CGTAAAAACT 500
 TAGACTACGC TCAAGCTGGT GACAACATCG GTGCATTATT ACGTGGTGTT 550
 CAACGTGAAG ACATCCAACG TGGTCAAGTA TTGGCTGCTC CTGGTTCAAT 600
 40 CACTCCACAT ACTAAATTTA AAGCGCAAGT TTACGTTTTA TCTAAAGAAG 650
 AAGGTGGACG TCATACACCA TTCTTAACTA ACTACCGTCC ACAATTCTAC 700
 TTCCGTACTA CTGACATTAC TGGTGTTATC ACTTTACCAG AAGACGTAGC 750
 TATGGTTATG CCTGGTGACA ACGTTGATAT GGACGTTGAA TTGATTCAAC 800
 CAGTTGCGAT CGAAGATGGT ACTAAATTCT CTATC 835

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2) INFORMATION FOR SEQ ID NO: 4

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Achromobacter xylosoxidans* subsp. *denitrificans*

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(B) STRAIN: ATCC 15173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

5	CCTGGTGGTG	TCGGCCGCTG	ACGGCCCCGAT	GCCGCAAACG	CGCGAACACA	50
	TCCTGCTGAG	CCGCCAGGTT	GGCGTGCCGT	ACATCATCGT	CTTCCTGAAC	100
	AAGGCCGACA	TGGTTGACGA	CGCCGAGCTG	CTTGAGCTGG	TGGAAATGGA	150
	AGTTCGCGAR	CTGCTGAGCA	AGTACGACTT	CCCGGGCGAC	GACACCCCGA	200
	TCGTGAAGGG	TTCGGCCAAG	CTGGCGCTGG	AAGGCGACAA	GGGCGAACTG	250
10	GGCGAACAGG	CCATCATGGC	GCTGGCCGCT	GCGCTGGACT	CGTACATCCC	300
	GACGCCTGAG	CGTGCCGTTG	ACGGCGCGTT	CCTGATGCCG	GTTGAAGACG	350
	TGTTCTCGAT	CTCGGGTCGC	GGCACCCTGG	TGACCGGCCG	TATCGAACGC	400
	GGCATCATCA	AGGTCGGCGA	GGAAATCGAA	ATCGTCGGTC	TGGTGCCGAC	450
	GGTGAAGACG	ACCTGCACGG	GCGTGGAAT	GTTCCGCAAG	CTGCTGGACC	500
15	AAGGTCAAGC	CGGCGACAAC	GTGGGCATCC	TRCTGCGCGG	CACCAAGCGT	550
	GAAGACGTCC	AGCGCGGCCA	GGTTCCTGGCC	AAGCCGGGCT	CGATCACCCC	600
	GCACACGGAC	TTCACGTCCG	AGGTGTACAT	CCTGTCCAAG	GAAGAAGGCG	650
	GCCGTCACAC	TCCGTTCTTC	CAAGGCTATC	GTCCCCAGTT	CTACTTCCGC	700
	ACGACGGACG	TGACGGGCAC	GATCGAGCTG	CCGGCCGACA	AGGAAATGGT	750
20	CCTGCCGGGC	GACAACGTGG	CCATGACGGT	CAAGCTGCTG	GCTCCGATCG	800
	CCATGGAAGA	AGGCCTGCGT	TCGCCAC			827

25 2) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 823 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Anaerorhabdus furcosus</i>
(B)	STRAIN: ATCC 25662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

40	TGGATCAATC	CTAGTAGTTG	CTGCAACTGA	TGGACCAATG	CCTCAAACCTC	50
	GTGAACATAT	CTTACTTGCT	CGTCAAGTAG	GTGTTCCAAG	AATGGTTGTA	100
	TTCTTGAACA	AATGCGACAT	GGTTGAAGAT	GAAGAATTAA	TCGACCTTGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTAAGTGC	TTACGGTTTC	GAAGGTGATG	200
45	ATACACCAGT	TATCCGTGGT	TCTGCATTAA	AATCTCTTGA	AGGAAATGCT	250
	GATTGGGAAG	CAAAAGTTGC	TGAATTAATG	GATGCAGTTG	ACTCTTGGAT	300
	TCCAACCTCA	ACTCATGAAA	CAGACAAACC	ATTCTTAATG	GCTGTTGAAG	350
	ATGTATTAC	AATTACAGGT	CGTGGTACAG	TTGCTACTGG	ACGTGTTGAA	400
	CGTGGACACT	TAAACCTTAA	CGAAGAAGTT	GAAATCGTTG	GTATTCATGA	450
50	TACTAAGAAA	TCAGTTGTTA	CTGGTATCGA	AATGTTCCGT	AAATTATTAG	500
	ACTATGCTGA	AGCAGGAGAC	AACATTGGTG	CATTATTACG	TGGTGTTTCT	550
	CGTGATGAAA	TCGAACGTGG	ACAATGTCTA	GCTAAACCTG	GATCAGTTAC	600
	TCCACATACA	GCTTTCAAAG	CTCAAGTATA	CGTATTAACT	AAAGAAGAAG	650
	GTGGACGTCA	TACACCATTTC	GTAACCTAAT	ACCGTCCTCA	ATTCTATTTC	700
55	CGTACAACCTG	ACGTAACAGG	AGTTGTATAA	CTTCCTGAAG	GTAAGTAAAT	750
	GGTTATGCCT	GGAGACAACA	TCGAAATGAT	CGTTGAATTA	ATCGCTCCAA	800
	TCGCTGTTGA	ACAAGGAACT	AAG			823

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2) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: 4229

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

CGGCGGTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCTCAAACCTC 50
 GTGAGCACAT CCTTCTTTCT CGTCAAGTAG GTGTACCTTA CATCGTTGTA 100
 TTCTTAAACA AATGCGACAT GGTAGACGAC GAAGAATTAT TAGAATTAGT 150
 20 AGAAATGGAA GTTCGCGACC TATTATCTGA ATACGGATTC CCAGGCGACG 200
 ACATTCCTGT AATCAAAGGT TCTGCTCTTA AAGCTCTTCA AGGAGAAGCT 250
 GATTGGGAAG CAAAAATCAT TGAATTAATG GCTGAAGTTG ATGCTTACAT 300
 CCCAACTCCA GAACGTGAAA CTGACAAACC ATTCTTAATG CCTGTAGAGG 350
 ACGTATTCTC TATCACAGGT CGTGGTACAG TTGCTACTGG TCGTGTTGAG 400
 25 CGCGGTATCG TTAAAGTTGG TGACGTAGTA GAAATCATCG GTCTTGCTGA 450
 AGAAAAATGCT TCTACAACCTG TAACTGGTGT AGAGATGTTC CGTAAACTTC 500
 TTGACCAAGC TCAAGCTGGA GACAACATCG GTGCTTTACT TCGTGGGGTT 550
 GCTCGTGAAG ACATCCAACG TGGACAAGTA CTTGCAAAAA GCGGTTCTGT 600
 AAAAGCTCAC GCTAAATTCA AAGCTGAAGT TTTCGTATTA TCTAAAGAAG 650
 30 AAGGTGGACG TCACACTCCA TTCTTCGCTA ACTACCGTCC TCAGTTCTAC 700
 TTCCGTACAA CTGACGTAAC TGGTATCATC CAATTACCAG AAGGTACTGA 750
 AATGGTAATG CCTGGTGACA ACATCGAAAT GACTATCGAA CTTATCGCTC 800
 CAATCGCTAT CGAAGAGGGA ACTAA 825

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2) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 14579

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

CGGCGGTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCTCAAACAC 50
 GTGAGCACAT CCTTCTTTCT CGTCAAGTAG GTGTTCTTA CATCGTTGTA 100
 55 TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAATTAT TAGAATTAGT 150
 AGAAATGGAA GTTCGCGACC TATTATCTGA ATACGGATTC CCAGGCGACG 200
 ACATTCCTGT AATCAAAGGT TCTGCTCTTA AAGCTCTTCA AGGAGAAGCT 250
 GATTGGGAAG CAAAAATCAT TGAATTAATG GCTGAAGTTG ATGCTTACAT 300
 CCCAACTCCA GAACGTGAAA CTGACAAACC ATTCTTAATG CCTGTAGAGG 350
 60 ACGTATTCTC TATCACAGGT CGTGGTACAG TTGCTACTGG TCGTGTTGAG 400

	CGCGGTATCG	TTAAAGTTGG	TGACGTAGTA	GAAATCATCG	GTCTTGCTGA	450
	AGAAAAATGCT	TCTACAAC TG	TAAC TGGTGT	AGAGATGTTT	CGTAAACTTC	500
	TTGACCAAGC	TCAAGCTGGA	GACAACATCG	GTGCTTTACT	TCGTGGGGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	CTTGCAAAAA	GCGGTTCTGT	600
5	AAAAGCTCAC	GCTAAATTCA	AAGCTGAAGT	TTTCGTATTA	TCTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCGCTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTATCATC	CAATTACCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGACA	ACATTGAAAT	GACTATCGAA	CTTATCGCTC	800
	CAATCGCTAT	CGAAGAGGGA	ACTAAATTC			829
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2) INFORMATION FOR SEQ ID NO: 8

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 818 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacteroides distasonis*

(B) STRAIN: ATCC 8503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

	CGGTGCTATC	ATCGTAGTTG	CTGCTACTGA	TGGTCCTATG	CCTCAAAC TC	50
30	GCGAGCACAT	CCTTTTGGCT	CGTCAGGTAA	ACGTTCCGAG	ATTGGTTGTA	100
	TTCATGAACA	AGTGTGACAT	GGTTGACGAC	GAGGAAATGT	TGGAATTGGT	150
	TGAGATGGAG	ATGAGAGAGT	TGCTTTCATT	CTATCAATTC	GACGGTGACA	200
	ACACTCCGAT	CATCCGTGGT	TCTGCTCTTG	GTGCATTGAA	CGGTGATGCT	250
	CAATGGGAAG	ATAAAGTAAT	GGAGTTGATG	GAAGCTTGTG	ATACTTGAT	300
35	TCCTCTGCCT	CCGCGCGAAA	TCGACAAGCC	GTTCTTGATG	CCGGTTGAGG	350
	ACGTATTCTC	AATCACGGGT	CGTGGTACTG	TTGCTACAGG	TCGTATCGAG	400
	ACAGGTATTG	TTAAGGTTGG	TGAGGAAGTT	CAGATCATCG	GTCTTGCGCG	450
	TGCTGGTAAG	AAATCTGTTG	TTACAGGTGT	TGAGATGTTC	CGTAAGTTAT	500
	TGGATCAAGG	TGAGGCTGGT	GATAACGTTG	GTTTGTTGCT	TCGCGGTATC	550
40	GATAAGAATG	AGATCAAGCG	TGGTATGGTA	ATCTGCCACC	CGGGTCAGGT	600
	TAAAGAGCAT	TCTAAGTTCA	AGGCTGAGGT	TTATATCTTG	AAGAAAGAGG	650
	AAGGTGGTCG	TCACACTCCG	TTCCACAACA	AATATCGTCC	TCAGTTCTAT	700
	ATCCGTACAT	TGGATGTAAC	TGGTGAGATC	ACTTTGCCGG	AAGGAACTGA	750
	AATGGTAATG	CCGGGTGATA	ACGTAACGAT	CGAGGTTGAG	TTGATCTATC	800
45	CGGTAGCATG	TAGCGTAG				818

2) INFORMATION FOR SEQ ID NO: 9

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 639 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

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5  GGTCCCTATGC CTCAAACACG TGAACACATC TTGTTATCAC GTAACGTTGG      50
   TGTACCATAC ATCGTTGTTT TCTTAAACAA AATGGATATG GTTGATGACG      100
   AAGAATTACT AGAATTAGTT GAAATGGAAG TTCGTGACTT ATTGTCAGAA      150
   TATGACTTCC CAGGCGACGA TGTTCTTGTA ATCGCTGGTT CTGCTTTGAA      200
   AGCTCTTGAA GCGGATGCTT CATACGAAGA AAAAATCATG GAATTAATGG      250
10  CTGCAGTTGA CGAATACGTT CCAACTCCAG AACGTGACAC TGACAAACCA      300
   TTCATGATGC CAGTCGAAGA CGTATTCTCA ATCACTGGAC GTGGTACTGT      350
   TGCTACAGGC CGTGTTGAAC GTGGACAAGT TCGCGTTGGT GACGAAGTTG      400
   AAATCGTTGG TATTGCTGAA GAAACTGCTA AAACAACGTG AACTGGTGTT      450
   GAAATGTTCC GTAAATTGTT AGACTATGCT GAAGCAGGGG ATAACATTGG      500
15  TGCATTGCTA CGTGGTGTTG CTCGTGAAGA CATCCAACGT GGACAAGTAT      550
   TGGCTAAAGC TGGTACAATC ACACCTCATA CAAAATTTAA AGCTGAAGTT      600
   TACGTTTTTAA CAAAAGAAGA AGGTGGACGT CACACACCA      639

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2) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

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25  (A) LENGTH: 692 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

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   (A) ORGANISM: Staphylococcus saprophyticus
   (B) STRAIN: CSG 197

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35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

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   GAACACATTC TTTTATCACG TAACGTTGGT GTTCCAGCAT TAGTTGTATT      50
   CTTAAACAAA GTTGACATGG TTGACGATGA AGAATTATTA GAATTAGTAG      100
   AAATGGAAGT TCGTGACTTA TTAAGCGAAT ATGACTTCCC AGGTGACGAT      150
40  GTACCTGTAA TCTCTGGTTC TGCATTAAAA GCTTTAGAAG GCGACGCTGA      200
   CTATGAGCAA AAAATCTTAG ACTTAATGCA AGCTGTTGAT GACTTCATTC      250
   CAACACCAGA ACGTGATTCT GACAAACCAT TCATGATGCC AGTTGAGGAC      300
   GTATTCTCAA TCACTGGTCG TGGTACTGTT GCTACAGGCC GTGTTGAACG      350
   TGGTCAAATC AAAGTCGGTG AAGAAATCGA AATCATCGGT ATGCAAGAAG      400
45  AATCAAGCAA AACAACTGTT ACTGGTGTAG AAATGTTCCG TAAATTATTA      450
   GACTACGCTG AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGTTC      500
   ACGTGATGAC GTACAACGTG GTCAAGTTTT AGCTGCTCCT GGTACTATTA      550
   CACCACATAC AAAATTCAA GCGGATGTTT ACGTTTTATC TAAAGATGAA      600
   GGTGGTCGTC ATACACCATT CTTCACTAAC TACCGCCAC AATTCTATTT      650
50  CCGTACTACT GACGTAAGTGT GTGTTGTAA CTTACCAGAA GG      692

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2) INFORMATION FOR SEQ ID NO: 11

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(i) SEQUENCE CHARACTERISTICS:

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60  (A) LENGTH: 821 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacteroides ovatus*
(B) STRAIN: ATCC 8483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11

10	CGGTGCTATC	ATCGTTTGTG	CTGCAACTGA	TGGTCCGATG	CCTCAAACCTC	50
	GCGAACACAT	TCTGTTAGCT	CGTCAGGTAA	ACGTACCTCG	TCTGGTTGTA	100
	TTCTTGAACA	AATGCGATAT	GGTAGACGAC	GAAGAAATGT	TGGAACCTCGT	150
	TGAAATGGAA	ATGAGAGAAC	TCCTTTCATT	CTATGATTTC	GATGGTGACA	200
	ATACTCCTAT	CATCCGTGGT	TCTGCTCTTG	GCGCATTGAA	CGGTGTTGAA	250
15	AAATGGGAAG	ACAAAGTTAT	GGAAGTATG	GATGCAGTTG	ATAACTGGAT	300
	TCCACTGCCT	CCGCGCGATG	TTGATAAACC	ATTCTTGATG	CCGTTTGAAG	350
	ACGTGTTCTC	TATCACAGGT	CGTGGTACTG	TAGCAACAGG	TCGTATCGAA	400
	ACAGGTGTCA	TCCACGTTGG	TGATGAAGTC	GAAATTCTTG	GTTTAGGTGA	450
	AGATAAGAAA	TCAGTTGTAA	CTGGTGTGTA	AATGTTCCGT	AAACTGTTGG	500
20	ATCAAGGTGA	AGCTGGTGAC	AACGTAGGTC	TTTGCTTCG	TGGTATTGAC	550
	AAGAACGAAA	TCAAACGTGG	TATGGTTCTT	TGTAAACCAG	GTCAGATTAA	600
	ACCGCACTCT	AAATTCAAAG	CTGAGGTTTA	TATCTTGAAG	AAAGAAGAAG	650
	GTGGTCGTCA	CACTCCGTTT	CACAACAAAT	ACCGTCCTCA	GTTCTACTTG	700
	CGTACTATGG	ACTGTACAGG	TGAAATCACT	TTGCCGGAAG	GAACAGAAAT	750
25	GGTAATGCCG	GGTGATAACG	TAACATATTAC	AGTTGAGTTG	ATTTACCCAG	800
	TAGCATTGAA	CCCGGGCTTC	G			821

30 2) INFORMATION FOR SEQ ID NO: 12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 838 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bartonella henselae*
(B) STRAIN: ATCC 49882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12

45	TGGTGCGATT	TTGGTTGTTT	CAGCTGCTGA	TGGTCCGATG	CCTCAAACAC	50
	GTGAGCATAT	TCTTCTTGCC	CGTCAGGTTG	GTGTTCCAGC	GATTGTTGTT	100
	TTTCTTAATA	AGGTTGATCA	GGTTGATGAT	GCTGAGCTTT	TGGAGCTTGT	150
	TGAGCTTGAA	GTTTCGGGAGT	TATTGTGCGAA	ATATGATTTT	CCAGGAGACG	200
50	ATATTCCGAT	CGTTAAAGGT	TCTGCTTTGG	CAGCGCTTGA	AGATAAAGAT	250
	AAAAGCATTG	GTGAAGATGC	GGTTCGTCTT	TTGATGAGTG	AAGTTGATAA	300
	TTATATACCG	ACGCCTGAAC	GTCCTGTTGA	TCAGCCGTTT	TTGATGCCAA	350
	TTGAAGATGT	TTTTTTCGATT	TCGGGTCGTG	GAAGTTGTGT	GACGGGTCGT	400
	GTTGAGCGTG	GTGTTATTAA	GGTTGGTGAA	GAAGTTGAGA	TTATCGGCAT	450
55	TCGTCCAAC	TCTAAGACAA	CAGTTACAGG	GGTTGAAATG	TTCCGCAAGC	500
	TTTTAGATCA	GGGGCAAGCG	GGTGATAATA	TTGGAGCGCT	GCTTCGTGGT	550
	ATTGATCGTG	AAGGGATTGA	GCGTGGACAA	GTTTTGGCGA	AGCCTGCTTC	600
	GGTTACACCT	CATACGAGAT	TAAAGCAGA	GGCTTACATT	TTGACGAAAG	650
	ATGAAGGTGG	TCGTCATACT	CCATTTTTC	CGAATTATCG	TCCTCAGTTT	700
60	TATTTCCGTA	CTACGGATGT	AACGGGAATT	GTTACGCTTC	CAGAAGGTAC	750

AGAGATGGTT ATGCCTGGTG ATAATGTTGC TATGGATGTC TCTCTGATTG 800
TTCCAATTGC CATGGAAGAA AAAC TTCGTT TTGCTATC 838

5

2) INFORMATION FOR SEQ ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 839 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium adolescentis*
(B) STRAIN: ATCC 15703

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

TGGCGCCATC CTTGTTGTGG CCGCCACCGA CGGCCCGATG GCTCAGACCC 50
GCGAGCACGT GCTGCTCGCT CGTCAGGTGG GCGTCCCGAA GATCCTCGTC 100
GCTCTGAACA AGTGCGATAT GGTCGACGAC GACGAGCTCA TCGAGCTCGT 150
25 TGAGGAAGAG GTCCGTGACC TCCTCGACGA AAATGGCTTC GATCGCGATT 200
GCCCGGTCAT CCACGTGTCC GCTTACGGCG CACTGCACGA TGACGCTCCG 250
GACCACGAGA AGTGGGTTGA GCAGATCAAG AAGCTCATGG ACGCCGTCGA 300
TGACTACATC CCGACCCCGG TCCACGATCT GGACAAGCCG TTCCTGATGC 350
CGATCGAAGA TGTCTTCACC ATCTCCGGCC GTGGCACCGT GGTGACCGGC 400
30 CGTGTGAGC GTGGTAAGCT CCCGGTCAAC TCCAACGTCG AGATCGTCGG 450
CATCCGTCCG ACCCAGACCA CCACCGTCAC CTCCATCGAG ACCTTCCACA 500
AGCAGATGGA CGAGTGCGAG GCTGGCGACA ACACCGGTCT GCTGCTCCGC 550
GGCATCAACC GTGACCAGGT CGAGCGTGGC CAGGTTCTGG CTGCTCCGGG 600
CTCCGTGACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA 650
35 AGGACGAAGG CGGCCGTCAC TCGCCGTTCT TCTCCAATA CCGTCCGCAG 700
TTCTACTTCC GTACCACCGA CGTCACCGGC GTCATCACCC TGCCGGAAGG 750
CGTTGAGATG GTGCAGCCGG GCGATCACGC TACCTTCGGC GTTGAGCTGA 800
TCCAGCCGAT CGCTATGGAA GAGGGCCTGA CCTTCGCAG 839

40

2) INFORMATION FOR SEQ ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 839 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium dentium*
(B) STRAIN: ATCC 27534

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

TGGCGCTATC CTCGTTGTGG CCGCCACCGA CGGCCCGATG GCTCAGACCC 50
GCGAGCACGT GCTGCTCGCT CGTCAGGTGG GCGTGCCGCG TATCCTCGTC 100
60 GCCCTGAACA AGTGCGATAT GGTCGACGAC GAAGAGCTCA TCGAGCTCGT 150

	TGAGGAAGAG	GTCCGTGACC	TCCTCGACGA	AAACGGCTTC	GATCGCGATT	200
	GCCCGGTCAT	CCACACCTCC	GCCTACGGCG	CGCTGCACGA	TGACGCTCCG	250
	GACCACGACA	AGTGGGTTGA	GTCCGTCAAG	GAACATCATGA	AGGCCGTCGA	300
	CGAGTACATC	CCGACCCCGA	CCCACGATCT	GGACAAGCCG	TTCCTGATGC	350
5	CGATCGAAGA	TGTGTTCAAC	ATCTCCGGCC	GTGGCACCGT	GGTTACCGGC	400
	CGTGTCGAGC	GTGGTAAGCT	CCCGGTCAAC	TCCAACGTTG	AGATCGTCGG	450
	CATCCGTCCG	ACCCAGACCA	CCACCGTCAC	CTCCATCGAG	ACCTTCCACA	500
	AGCAGATGGA	CGAGTGCGAG	GCTGGCGACA	ACACCGGTCT	GCTGCTCCGC	550
	GGCATCAACC	GTGACCAGGT	CGAGCGTGGC	CAGGTTCTGG	CTGCTCCGGG	600
10	CTCCGTGACC	CCGCACACCA	AGTTCGAGGG	CGAAGTCTAC	GTGCTGACCA	650
	AGGACGAAGG	CGGCCGTCAC	TCGCCGTTCT	TCTCCAACTA	CCGTCCGCAG	700
	TTCTACTTCC	GTACCACCGA	CGTCACCGGC	GTCATCACCC	TGCCGGAAGG	750
	CGTTGAGATG	GTGCAGCCGG	GCGATCACGC	TACCTTCGGC	GTTGAGCTGA	800
	TCCAGCCGAT	CGCTATGGAA	GAGGGCCTGA	CCTTCGCAG		839

2) INFORMATION FOR SEQ ID NO: 15

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 838 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Brucella abortus*

30 (B) STRAIN: S2308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

	TGGCGCGATC	CTGGTGGTTT	CGGCTGCTGA	CGGCCCGATG	CCGCAGACCC	50
35	GCGAGCACAT	CCTGCTTGCC	CGTCAGGTTG	GCGTTCCGGC	GATCGTCGTG	100
	TTCTTCAACA	AGTGCGACCA	GGTTGACGAT	GCAGAACTGC	TCGAACTGGT	150
	TGAACTGGAA	GTGCGCGAAC	TTCTGTGCGA	GTACGAATTC	CCCGGCGACG	200
	AAATCCCGAT	CATCAAGGGC	TCGGCTCTTG	CTGCTCTGGA	AGATTCTTCC	250
	AAGGAAGTGG	GCGAAGATGC	CATCCGCAAC	CTGATGGACG	CGGTTGACAG	300
40	CTACATTCCG	ACCCCGGAAC	GCCCGATCGA	CCAGCCGTTT	CTGATGCCGA	350
	TCGAAGACGT	GTTCTCGATC	TCCGGCCGTG	GTACGGTTGT	GACGGGTCGC	400
	GTGAGCGCG	GTATCGTTAA	GGTCGGTGAA	GAAGTTGAAA	TGGTCGGCAT	450
	CAAGGCGACG	ACGAAGACCA	CGGTTACCGG	CGTTGAAATG	TTCCGCAAGC	500
	TGCTCGACCA	GGGCCAGGCT	GGCGACAACA	TTGGCGCGCT	GATCCGCGGC	550
45	GTTGGCCGTG	AAGACGTTGA	ACGCGGCCAG	GTTCTCTGCA	AGCCGGGTTT	600
	TGTGAAGCCG	CACACCAAGT	TTAAGGCAGA	AGCCTATATT	CTGACCAAGG	650
	ACGAAGGTGG	CCGTCATACG	CCGTTCTTCA	CCAACATCCG	TCCGCAGTTC	700
	TACTTCCGTA	CGACGGACGT	GACGGGTGTT	GTGACGCTTC	CGGCTGGCAC	750
	GGAAATGGTC	ATGCCTGGCG	ATAACGTCGC	CATGGACGTT	ACCCTGATCG	800
50	TGCCGATCGC	CATGGAAGAG	AAGCTTCGCT	TCGCTATC		838

2) INFORMATION FOR SEQ ID NO: 16

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 771 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Burkholderia cepacia*
(B) STRAIN: LSPQ 2217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

10	GGCAGCAGAC	GGCCCGATGC	CGCAAACGCG	TGAGCACATC	CTGCTGGCGC	50
	GTCAGGTTGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	GTGCGACATG	100
	GTGGACGACG	CCGAACGTCT	CGAGCTGGTC	GAGATGGAAG	TTCGCGAACT	150
	CCTGTCGAAG	TACGACTTCC	CGGGCGACGA	CACGCCGATC	GTGAAGGGTT	200
	CGGCGAAGCT	GGCGCTGGAA	GGCGACACGG	GCGAGCTGGG	CGAAGTGGCG	250
15	ATCATGAGCC	TGGCCGACGC	GCTGGACACG	TACATCCCGA	CGCCGGAGCG	300
	TGCAGTTGAC	GGCGCGTTCC	TGATGCCGGT	GGAAGACGTG	TTCTCGATCT	350
	CGGGCCGCGG	TACGGTGGTG	ACGGGTCGTG	TCGAGCGCGG	CATCGTGAAG	400
	GTCGGCGAAG	AAATCGAAAT	CGTCGGTATC	AAGCCGACGG	TGAAGACGAC	450
	CTGCACGGGC	GTTGAAATGT	TCCGCAAGCT	GCTGGACCAA	GGTCAAGCAG	500
20	GCGACAACGT	TGGTATCCTG	CTGCGCGGCA	CGAAGCGTGA	AGACGTGGAG	550
	CGTGGCCAGG	TTCTGGCGAA	GCCGGGTTCG	ATCACGCCGC	ACACGCACTT	600
	CACGGCTGAA	GTGTACGTGC	TGAGCAAGGA	CGAAGGCGGC	CGTCACACGC	650
	CGTTCTTCAA	CAACTACCGT	CCGCAGTTCT	ACTTCCGTAC	GACGGACGTG	700
	ACGGGCTCGA	TCGAGCTGCC	GAAGGACAAG	GAAATGGTGA	TGCCGGGCGA	750
25	CAACGTGTCG	ATCACGGTGA	A			771

2) INFORMATION FOR SEQ ID NO: 17

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Cedecea davisae*
(B) STRAIN: ATCC 33431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

45	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAT	GGCCCAATGC	CACAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTTGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGTGAACT	TCTGTCCCAG	TACGACTTCC	CGGGCGACGA	200
	TACTCCAATC	GTTTCGTGGT	CTGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
50	AGTGGGAAGC	TAAAATCGTT	GAGCTGGCTG	GCTACCTGGA	TTCTTACATC	300
	CCTGAGCCAG	AGCGTGCTAT	CGATAAGCCG	TTCTTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGCC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAT	450
	ACTGCGAAAT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
55	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCAGG	CTCTATCAAG	600
	CCACACACCA	AGTTCGAATC	TGAAGTGTAC	ATCCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACCTGA	CGTGACCGGC	ACCATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
60	GTAATGCCTG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCAAT	800

CGCGATGGAT GACGGTCTGC GTTTCGCAA

5 2) INFORMATION FOR SEQ ID NO: 18

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea neteri*
 (B) STRAIN: ATCC 33855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18

20 CGCTATCCTG GTTGTGCTG CGACTGACGG CCCTATGCCT CAGACCCGTG 50
 AGCACATCCT GCTGGGTCGT CAGGTTGGCG TTCCTTACAT CATCGTGTTC 100
 CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTTGA 150
 AATGGAAGTT CGTGAAGTTC TGTCTCAGTA CGACTTCCCG GGCGATGACA 200
 25 CTCCAATCAT CCGTGTTTCT GCTCTGAAAG CGCTGGAAGG CGAAGCAGAG 250
 TGGGAAGCTA AAATYGTGA GCTGGCTGGC TTCCTGGATT CCTACATCCC 300
 AGAACCAGTA CGTGCAATCG AYCTGCCGTT CCTGCTGCCA ATCGAAGACG 350
 TATTCTCCAT CTCCGGCCGT GGTACCGTTG TTACCGGTCG TGTAGAGCGC 400
 GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATAC 450
 30 TGCGAAATCT ACCTGTACCG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG 500
 AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAACGT 550
 GAAGAAATCG AACGTGGTCA GGTCTCTGGCT AAGCCAGGCT CTATCAAGCC 600
 GCACACCAAG TTCGAATCTG AAGTGACAT CCTGTCCAAA GACGAAGGCG 650
 GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCACAGTT CTACTTCCGT 700
 35 ACAACTGACG TGACCGGTAC CATCGAACTG CCAGAAGGCG TAGAGATGGT 750
 AATGCCAGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG 800
 CGATGGACGA CGGTCTGCGT TTCG 824

40

2) INFORMATION FOR SEQ ID NO: 19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea lapagei*
 (B) STRAIN: ATCC 33432

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19

CGCTATTCTG GTTGTGCTG CAACTGACGG CCCTATGCCT CAGACCCGTG 50
 AGCACATCCT GCTGGGTCGC CAGGTTGGCG TTCCTTACAT CATCGTGTTC 100
 CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTAGA 150
 60 AATGGAAGTT CGTGAAGTTC TGTCTCAGTA CGACTTCCCA GGCGATGATA 200

	CCCCAATCAT	CCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGAAGCAGAG	250
	TGGGAAGCTA	AAATCGTTGA	GCTGGCTGGC	TTCCTGGATT	CCTACATCCC	300
	AGAACCAGTA	CGTGCAATCG	ACCTGCCGTT	CCTGCTGCCA	ATCGAAGACG	350
	TATTCTCCAT	CTCCGGCCGT	GGTACCGTTG	TKACCGGTCG	TGTAGAGCGC	400
5	GGTATCGTTA	AAGTGGGCGA	AGAAGTAGAA	ATCGTTGGTA	TCAAAGATAC	450
	TGCGAAATCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGACG	500
	AAGGCCGTGC	TGGTGAGAAC	GTTGGTGTTT	TGCTGCGTGG	TATCAAACGT	550
	GAAGAAATCG	AACGTGGTCA	GGTTCTGGCT	AAGCCAGGCT	CTATCAAGCC	600
	GCACACCAAG	TTCGAATCTG	AAGTGTACAT	CCTGTCCAAA	GACGAAGGCG	650
10	GCCGTCATAC	TCCGTTCTTC	AARGGCTACC	GTCCACAGTT	CTACTTCCGT	700
	ACCACTGACG	TGACCGGTAC	CATCGAACTG	CCAGAAGGCG	TAGAGATGGT	750
	AATGCCAGGT	GACAACATCA	AAATGGTTGT	TACCCTGATC	CACCCAATCG	800
	CGATGGACGA	CGGTCTGCGT	TTCGCAA			827

15

2) INFORMATION FOR SEQ ID NO: 20

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 831 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia pneumoniae*

(B) STRAIN: CWL 029

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

	GCGGAGCTAT	CCTAGTCGTT	TCAGCTACAG	ACGGAGCTAT	GCCACAAACT	50
	AAAGAACATA	TCTTGCTAGC	TCGCCAGGTT	GGAGTTCCTT	ATATCGTTGT	100
35	TTTCTTGAAT	AAAGTAGATA	TGATCTCTCA	AGAAGATGCT	GAAC TTATTG	150
	ACCTTGTTGA	GATGGA ACTT	AGTGAGCTTC	TTGAAGAAAA	AGGCTACAAA	200
	GGATGCCCTA	TTATCCGTGG	TTCTGCTTTG	AAAGCTCTTG	AAGGTGATGC	250
	AAATTATATC	GAAAAAGTTC	GAGAACTTAT	GCAAGCTGTG	GATGACAACA	300
	TCCCTACACC	AGAAAGAGAA	ATTGATAAGC	CTTTCTTAAT	GCCTATCGAA	350
40	GACGTATTCT	CAATCTCTGG	TCGTGGTACT	GTGGTTACAG	GAAGAATCGA	400
	GCGTGGAATC	GTTAAAGTTT	CTGATAAAGT	TCAGCTCGTG	GGATTAGGAG	450
	AGACTAAAGA	AACAATCGTT	ACTGGAGTCG	AAATGTTTCAG	GAAAGAACTT	500
	CCTGAAGGTC	GTGCAGGAGA	AAACGTTGGT	TTACTCCTCA	GAGGTATTGG	550
	AAAGAACGAT	GTTGAAAGAG	GTATGGTGGT	TTGTCAGCCT	AACAGCGTGA	600
45	AGCCTCATAC	GAAATTTAAG	TCAGCTGTTT	ACGTTCTTCA	GAAAGAAGAA	650
	GGCGGACGTC	ATAAGCCTTT	CTTCAGCGGA	TACAGACCTC	AGTTCTTCTT	700
	CCGTACTACA	GACGTGACAG	GAGTCGTAAC	TCTTCCTGAA	GGAAGTGAAG	750
	TGGTAATGCC	TGGAGATAAC	GTTGAGCTTG	ATGTTGAGCT	CATTGGAACA	800
50	GTTGCTCTTG	AAGAAGGAAT	GAGATTTGCA	A		831

2) INFORMATION FOR SEQ ID NO: 21

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia psittaci*

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21

	TGGAGCGATT	CTCGTTGTTT	CCGCTACTGA	CGGTGCGATG	CCTCAGACCA	50
	AAGAACATAT	TCTTTTGCG	AGACAGGTTG	GTGTTCTTA	CATCGTTGTT	100
10	TTCCTTAACA	AAATCGATAT	GATTTCTCAA	GAAGATGCTG	AGCTCGTAGA	150
	CTTAGTTGAA	ATGGAATTGT	CCGAACCTCT	AGAAGAAAAA	GGTTATAAAG	200
	GTTGCCCAAT	TATCCGTGGT	TCTGCTTTGA	AAGCCTTAGA	AGGTGATGCA	250
	AGCTACGTTG	AAAAAATTCG	CGAGTTAATG	CAAGCAGTGG	ATGATAACAT	300
	CCCTACTCCA	GAGCGTGAAG	TTGATAAGCC	TTTCTTAATG	CCTATCGAAG	350
15	ACGTATTCTC	TATTTCTGGT	CGTGGTACTG	TGGTCACAGG	ACGTATCGAG	400
	CGTGGAATCG	TTAAAGTGGG	TGATAAAGTA	CAGATTGTTG	GTTTAAGAGA	450
	TACTAGAGAG	ACAATTGTTA	CCGGTGTGGA	AATGTTTCTG	AAAGAAGTTC	500
	CAGAAGGTCA	AGCAGGGGAA	AACGTTGGTT	TGCTCCTCAG	AGGTATCGGT	550
	AAGAATGACG	TTGAACGTGG	TATGGTTATC	TGCCAACCTA	ATAGCGTGAA	600
20	ATCTCACACA	CAATTTAAAG	GTGCTGTCTA	CATTCTACAA	AAAGAAGAGG	650
	GTGGACGTC	TAAACCTTTC	TTTACCGGAT	ACAGACCTCA	GTTCTTCTTC	700
	CGTACAACAG	ATGTTACAGG	TGTTGTAAC	CTCCCAGAA	GTACAGAGAT	750
	GGTTATGCCA	GGCGATAACG	TTGAATTCGA	AGTTCAATTA	ATTAGCCAG	800
	TAGCTCTAGA	AGAAGGTATG	AGATTT			826

25

2) INFORMATION FOR SEQ ID NO: 22

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia trachomatis*

40

(B) STRAIN: LGV 12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22

	GGGGCTATTC	TAGTAGTTTC	TGCAACAGAC	GGAGCTATGC	CTCAAACATAA	50
45	AGAGCATATT	CTTTTGCCAA	GACAAAGTTG	GGTTCCTTAC	ATCGTTGTTT	100
	TTCTCAATAA	AATTGACATG	ATTTCCGAAG	AAGACGCTGA	ATTGGTCGAC	150
	TTGGTTGAGA	TGGAGTTGGC	TGAGCTTCTT	GAAGAGAAAG	GATACAAAGG	200
	GTGTCCAATC	ATCAGAGGTT	CTGCTCTGAA	AGCTTTTGAA	GGGGATGCTG	250
	CATACATAGA	GAAAGTTCTG	GAGCTAATGC	AAGCCGTCGA	TGATAATATC	300
50	CCTACTCCAG	AAAGAGAAAT	TGACAAGCCT	TTCTTAATGC	CCATTGAGGA	350
	CGTGTTCCTC	ATCTCCGGAC	GAGGAACTGT	AGTAACTGGA	CGTATTGAGC	400
	GTGGAATTGT	TAAAGTTTCC	GATAAAGTTC	AGTTGGTCGG	TCTTAGAGAT	450
	ACTAAAGAAA	CGATTGTTAC	TGGGGTTGAA	ATGTTTCAGAA	AAGAAGTCCC	500
	AGAAGGTCGT	GCAGGAGAGA	ATGTTGGATT	GCTCCTCAGA	GGTATTGGTA	550
55	AGAACGATGT	GGAAAGAGGA	ATGGTTGTTT	GCTTGCCAAA	CAGTGTTAAA	600
	CCTCATACAC	GGTTTAAGTG	TGCTGTTTAC	GTTCTGCAAA	AAGAAGAAGG	650
	TGGACGACAT	AAGCCTTTCT	TCACAGGATA	TAGACCTCAA	TTCTTCTTCC	700
	GTACAACAGA	CGTTACAGGT	GTGGTAACTC	TGCCTGAGGG	AGTTGAGATG	750
	GTCATGCCTG	GGGATAACGT	TGAGTTTGAA	GTGCAGTTGA	TTAGCCCTGT	800
60	GGCTTTAGAA	GAAGGTATGA	GA			822

15

2) INFORMATION FOR SEQ ID NO: 23

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chryseobacterium meningosepticum*
 (B) STRAIN: CDC B7681

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23

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20  CGGAGCTATC TTAGTATGTG CTGCTACAGA TGGTCCAATG CCTCAAACCTA      50
    GAGAACACAT CCTACTTTGC CGTCAGGTAA ACGTACCTAG AATTGTTGTG      100
    TTCATGAACA AAGTTGACAT GGTAGATGAT CCAGAATTGT TAGAGCTTGT      150
    TGAGCTTGAA CTTAGAGATC TATTATCTAC TTACGAATAT GATGGTGATA      200
    ACTCTCCAGT AATTCAAGGT TCTGCTCTTG GTGCTCTTAA CGGTGATGCT      250
25  AAGTGGGTAG CTACTGTAGA AGCTCTAATG GATGCTGTTG ATACTTGGAT      300
    CGAGCAACCA GTAAGAGATT CTGATAAGCC ATTCCTTATG CCAATCGAAG      350
    ACGTATTCTC TATTACAGGT AGAGGTAAGT TAGCAACTGG TAGAATCGAG      400
    GCTGGTGTA TCAACACAGG TGATCCTGTT GACATCGTAG GTATGGGTGA      450
    CGAGAAGTTA ACTTCTACTA TTACAGGTGT TGAGATGTTT AGAAAAATCC      500
30  TAGACAGAGG TGAAGCTGGT GATAACGTAG GTCTATTGTT GAGAGGTATT      550
    GAAAAGACTG ACATCAAGAG AGGTATGGTT ATCGCTAAGA AAGATTTCAGT      600
    TAAGCCACAC AAGAAATTCA AAGCTGAGGT TTATATCCTT TCTAAAGAAG      650
    AAGGTGGACG TCACACTCCA TTCCACAACA AATACCGTCC TCAGTTCTAT      700
    GTAAGAATA CTGACGTTAC AGGTGAAATC TTCTTACCAG AAGGTGTAGA      750
35  AATGGTAATG CCTGGTGATA ACTTAACTAT CACTGTAGAA TTGTTACAAC      800
    CAATCGCTCT TAACGAGGGT CTTAGATTCTG CGATC                      835
  
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40 2) INFORMATION FOR SEQ ID NO: 24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter amalonaticus*
 (B) STRAIN: ATCC 25405

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24

55

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    CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC      50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT      150
    AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTT CCGGGCGACG      200
60  ACACCCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA      250
  
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	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCC	GGCTTCCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
5	GA CTGCCAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCGGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCWCCATCAA	600
	GCCGCACACC	ATGTTCGAAT	CYGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
10	CGTACAAC TG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTTGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGG				816

15

2) INFORMATION FOR SEQ ID NO: 25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter braakii*

(B) STRAIN: ATCC 43162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25

	CGCGATCCTG	GTTGTTGCTG	CAACTGACGG	CCCGATGCCG	CAGACTCGTG	50
	AGCACATCCT	GCTGGGTCGY	CAGGTAGGCG	TTCCGTACAT	CATCGTGTTT	100
	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTAGA	150
35	AATGGAAGTT	CGTGAAC TTC	TGTCTCAGTA	CGATTTCCCG	GGCGACGACA	200
	CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGAWGCAGAG	250
	TGGGAAGCGA	AAATCATCGA	ACTGGCTGGC	TTCTGGAATT	CTTACATCCC	300
	GGAACCAGAG	CGTGCGATTG	ACAAGCCGTT	CCTGCTGCCT	ATCGAAGACG	350
	TATTCTCCAT	CTCTGGTTCG	GGTACCGTTG	TTACCGGTCT	TGTAGAGCGC	400
40	GGTATCATCA	AAGTTGGTGA	AGAAGTTGAA	ATCGTTGGTA	TCAARGACAC	450
	TGCTAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGACG	500
	AAGGCCGTGC	TGGTGAGAAC	GTTGGTGTTT	TGCTGCGTGG	TATCAAGCGT	550
	GAAGAAATCG	AACGTGGTCA	GGTACTGGCT	AAGCCGGGCT	CTATCAAGCC	600
	GCACACCAAG	TTCGAATCTG	AAGTGATACAT	TCTGTCCAAA	GACGAAGGCG	650
45	GCCGTCATAC	TCCGTTCTTC	AARGGCTACC	GTCCGCAGTT	CTACTTCCGT	700
	ACTACTGACG	TGACTGGTAC	CATCGAACTG	CCGGAAGGCG	TTGAGATGGT	750
	AATGCCGGGC	GACAACATCA	AAATGGTTGT	TACCCTGATC	CACCCAATCG	800
	CGATGGACGA	CGGTCTGCGT	TTCGC			825

50

2) INFORMATION FOR SEQ ID NO: 26

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter koseri*
 (B) STRAIN: ATCC 27156

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
10	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAGATGGAA	GTGCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ACACGCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAMGCT	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTACCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATYGTG	GTATCAAAGA	450
	GACTGCGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GYTCCATCAA	600
20	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATYCTGTCY	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAACTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
25	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA			830

2) INFORMATION FOR SEQ ID NO: 27

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter farmeri*
 (B) STRAIN: ATCC 51112

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27

	CGCGATCCTG	GTTGTTGCTG	CGACTGACGG	CCCGATGCCG	CAGACTCGTG	50
45	AGCACATCCT	GCTGGGTCGT	CAGGTAGGCG	TTCCGTACAT	CATCGTGTTT	100
	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTAGA	150
	GATGGAAGTT	CGTGAAGTGC	TGTCTCAGTA	CGATTTCCCG	GGCGACGACA	200
	CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGACGCAGAG	250
	TGGGAAGCGA	AAATCATCGA	ACTGGCAGGC	TTCTTGATT	CTTACATCCC	300
50	GGAACCAGAG	CGTGCGATTG	ACAAGCCGTT	CCTGCTGCCG	ATCGAAGACG	350
	TATTCTCCAT	CTCTGGTCGT	GGTACCGTTG	TTACCGGTCG	TGTAGAGCGC	400
	GGTATCATCA	AAGTGGGTGA	AGAAGTTGAA	ATCGTTGGTA	TCAAAGAGAC	450
	TGCCAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGACG	500
	AAGGCCGTGC	TGGTGAGAAC	GTAGGTGTTT	TGCTGCGTGG	TATCAAACGT	550
55	GAAGAAATCG	AACGTGGTCA	GGTACTGGCT	AAGCCGGGCW	CCATCAAGCC	600
	RCACACTATG	TTCGAATCTG	AAGTGACAT	TCTGTCCAAA	GACGAAGGCG	650
	GCCGTCATAC	TCCGTTCTTC	AAAGGCTACC	GTCCGCAGTT	CTACTTCCGT	700
	ACGACTGACG	TGACTGGCAC	CATCGAACTG	CCGGAAGGTG	TTGAGATGGT	750
	TATGCCGGGC	GACAACATCA	AAATGGTTGT	TACCCTGATC	CACCCGATCG	800
60	CGATGGACGA	CGGTCTGCGT	TTGCGCAA			827

2) INFORMATION FOR SEQ ID NO: 28

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter freundii*
 (B) STRAIN: ATCC 8090

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28

20	CCTGGTTGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACT	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCTG	ACATCATCGT	GTTCCCTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TAGAAATGGA	150
	AGTTCGTGAA	CTTCTGTCTC	AGTACGATTT	CCCGGGCGAC	GACACTCCGA	200
	TCGTTTCGTG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGAAGC	AGAGTGGGAA	250
25	GCGAAAATCA	TCGAACTGGC	TGGCTTCCTG	GATTCTTACA	TCCCAGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCTATCGAA	GACGTATTCT	350
	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTGCTAA	450
	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAGTCTG	GACGAAGGCC	500
30	GTGCTGGTGA	GAACGTTGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCTCTATCA	AGCCGCACAC	600
	CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGACGAA	GGCGGCCGTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACTACT	700
	GACGTGACTG	GTACCATCGA	ACTGCCGGAA	GGCGTAGAGA	TGGTAATGCC	750
35	GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCA	ATCGCGA	797

2) INFORMATION FOR SEQ ID NO: 29

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter sedlakii*
 (B) STRAIN: ATCC 51115

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29

55	CGGCGCGATC	CTGGTTGTTG	CCGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCTTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAGATGGAA	GTTTCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ACACGCCGAT	CGTTCGTGGT	TCAGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
60	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300

	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	G TTCCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
5	ACGAAGGCCG	TGCGGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCGAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	TATTCTGTCC	AAAGATGAAG	650
	GCGGCCCTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
10	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

15 2) INFORMATION FOR SEQ ID NO: 30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter werkmanii*
 (B) STRAIN: ATCC 51114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30

30	GCGATCCTGG	TTGTTGCTGC	GACTGACGGC	CCGATGCCGC	AGACTCGTGA	50
	GCACATCCTG	CTGGGTCGTC	AGGTAGGCGT	TCCGTACATC	ATCGTGTTCC	100
	TGAACAAATG	CGACATGGTT	GATGACGAAG	AGCTGCTGGA	ACTGGTAGAA	150
	ATGGAAGTTC	GTGAACTTCT	GTCTCAGTAC	GATTTCCTCG	GCGACGACAC	200
35	TCCGATCGTT	CGTGGTTCTG	CTCTGAAAGC	GCTGGAAGGC	GAAGCAGAGT	250
	GGGAAGCGAA	AATCATCGAA	CTGGCTGGCT	TTCTGGATTC	TTACATCCCG	300
	GAACCAGAGC	GTGCGATTGA	CAAGCCGTTT	CTGCTRCCTA	TCGAAGACGT	350
	ATTCTCCATC	TCCGGTCGTG	GTACCGTTGT	TACCGGTCGT	GTAAGACGCG	400
	GTATCATCAA	AGTTGGTGAA	GAAGTTGAAA	TCGTTGGTAT	CAAAGACACC	450
40	GCTAAGTCTA	CCTGTACCGG	CGTTGAAATG	TTCCGCAAAC	TGCTGGACGA	500
	AGGCCGTGCT	GGTGAGAACG	TTGGTGTTCT	GCTGCGTGGT	ATCAAACGTG	550
	AAGAAATCGA	ACGTGGTCAG	GTACTGGCTA	AGCCGGGCTC	TATCAAGCCG	600
	CACACCAAGT	TCGAATCTGA	AGTGATACAT	CTGTCCAAAG	ACGAAGGCGG	650
	CCGTCATACT	CCGTTCTTCA	AAGGCTACCG	TCCGCAGTTC	TACTTCCGTA	700
45	CTACTGACGT	GACTGGTACC	ATCGAACTGC	CGGAAGGCGT	AGAGATGGTA	750
	ATGCCGGGCG	ACAACATYAA	AATGGTTGTT	ACYCTGATCC	ACCCGATCGC	800
	GATGGACGAC	GGTCTGCGTT	TCG			823

50

2) INFORMATION FOR SEQ ID NO: 31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter youngae*

(B) STRAIN: ATCC 29935

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGCTGGTA	150
10	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTC	CGGGCGACGA	200
	TACGCCGATC	GTTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
	AGTGGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATC	300
	CCGGAACCAG	AACGTGCTAT	CGATAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACTGGT	CGTGTAGAAG	400
15	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCCAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCTATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGACGAAGG	650
20	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACGGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCAAT	800
	CGCGATGGAT	GACGGTCTGC	GTTTCG			826

25

2) INFORMATION FOR SEQ ID NO: 32

(i) SEQUENCE CHARACTERISTICS:

30	(A) LENGTH: 841 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium perfringens*

(B) STRAIN: ATCC 13124

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32

	CGGAGCTATA	TTAGTTTGT	CAGCAGCTGA	TGGTCCAATG	CCTCAAACAA	50
	GAGAGCACAT	CTTATTATCA	TCAAGAGTTG	GAGTTGACCA	CATCGTAGTA	100
45	TTCTTAAACA	AAGCAGATAT	GGTTGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTAGAGAGT	TATTAAGCGA	GTACAACTTC	CCAGGAGACG	200
	AYATTCCAGT	AATCAARGGA	TCAGCTTTAG	TAGCATTAGA	AAACCCCACT	250
	GACGAAGCTG	CAACAGCTTG	TATCAGAGAG	TTAATGGATG	CTGTAGATAG	300
	CTACATCCCA	ACACCAGAAA	GAGCAACAGA	TAAGCCATTC	TTAATGCCAG	350
50	TAGAGGACGT	ATTCACAATC	ACTGGTAGAG	GAACAGTTGC	AACAGGAAGA	400
	GTTGAAAGAG	GAGTTCTACA	TGTAGGAGAC	GAAGTAGAAG	TAATCGGATT	450
	AACTGAAGAA	AGAAGAAAAA	CTGTTGTAAC	AGGAATCGAA	ATGTTCAGAA	500
	AGTTATTAGA	TGAAGCACAA	GCTGGAGATA	ACATCGGAGC	ATTATTAAGA	550
	GGTATCCAAA	GAAGTAYAT	CGAAAGAGGT	CAAGTTTTAG	CTCAAGTTGG	600
55	AACAATCAAC	CCACACAAAA	AATTCGTAGG	TCAAGTATAC	GTACTTAAAA	650
	AAGAAGAAGG	TGGAAGACAT	ACTCCATTCT	TGCATGGATA	CAGACCACAA	700
	TTCTACTTCA	GAACAACAGA	CGTTACAGGA	TCAATCAAAT	TACCAGAAGG	750
	AATGGAAATG	GTTATGCCTG	GAGACCACAT	CGACATGGAA	GTTGAATTAA	800
	TCACAGAAAT	CGCTATGGAY	GAAGGATTAA	GATTCGCTAT	C	841

60

2) INFORMATION FOR SEQ ID NO: 33

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Comamonas acidovorans*
 15 (B) STRAIN: ATCC 15668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33

	CGGCGCCATC	CTGGTGTGCT	CGGCCGCTGA	CGGCCCCATG	CCCCAGACCC	50
20	GCGAGCACAT	CCTGCTGGCC	CGTCAGGTGG	GCGTGCCCTA	CATCATCGTG	100
	TTCCTGAACA	AGTGCGACAT	GGTGGACGAC	GAAGAGCTGC	TGGAAGTGGT	150
	CGAAATGGAA	GTGCGCGAGC	TGCTTGCCAA	GTACGACTTC	CCCGGCGACG	200
	ACACCCCATC	CATCCGCGGC	TCGGCCAAGC	TGGCCCTGGA	AGGCGACCAG	250
	TCCGACAAGG	GCGAACCTGC	CATCCTGCGC	CTGGCTGAAG	CACTGGACTC	300
25	CTACATCCCC	ACGCCCAGC	GCGCTGTGGA	CGGCGCCTTT	GCAATGCCCG	350
	TGGAAGACGT	GTTCTCGATC	TCTGGCCGTG	GCACCGTGGT	GACTGGCCGT	400
	ATCGAGCGCG	GCATCATCAA	GGTCGGCGAA	GAAATCGAAA	TCGTCGGTAT	450
	CCGCGACACC	CAGAAGACCA	TCGTCACCGG	CGTGGAAATG	TTCCGCAAGC	500
	TGCTGGACCA	AGGTCAAGCT	GGCGACAACG	TGGGTCTGCT	GCTGCGCGGC	550
30	ACCAAGCGTG	AAGACGTGGA	ACGCGGCCAA	GTGCTGTGCA	AGCCCGGCTC	600
	CATCAAGCCC	CACACCCACT	TCACGGCTGA	GGTGTACGTG	CTGTCCAAGG	650
	ACGAAGGTGG	TCGCCACACT	CCGTTCTTCA	ACAACCTACG	TCCCCAGTTC	700
	TATTTCCGTA	CGACCGACGT	GACCCGCTCC	ATCGAGCTGC	CCGCCGACAA	750
	GGAAATGGTG	ATGCCTGGCG	ACAACGTGTC	GATCACCGTC	AAGCTGATCG	800
35	CCCCCATCGC	CATGGAAGAA	GG			822

2) INFORMATION FOR SEQ ID NO: 34

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 702 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Corynebacterium bovis*
 (B) STRAIN: ATCC 7715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

55	GCCGCAGACC	CGTGAGCACG	TCCTCCTGGC	CCGTCAGGTC	GGTGTGCCCT	50
	ACATCCTCGT	CGCCCTCAAC	AAGTGCGACA	TGGTCGACGA	CGAGGACCTC	100
	ATCGAGCTCG	TCGAGATGGA	GGTCCGTGAG	CTCCTCGCCG	AGCAGGACTA	150
	CGACGAGGAC	GCCCCGATCA	TCCACATCTC	CGCCCTCAAG	GCCCTCGAGG	200
	GTGACCCGGA	GTGGACGCAG	CGCATCGTCG	ACCTCATGAA	GGCCTGCGAC	250
60	GACGCCATCC	CGGATCCGGA	GCGCGAGACG	GACAAGCCGT	TCCTCATGCC	300

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GATCGAGGAC ATCTTCACGA TCACCGGCCG CGGCACCGTC GTCACGGGCC 350
GTGTCGAGCG TGGCATCCTC AACGTCAACG AGGAGGTCGA GATCCTGGGT 400
ATCTGCGAGA ACTCCCAGAA GACGACCGTC ACCTCCATCG AGATGTTCAA 450
CAAGTTCCTC GACACGGCCG AGGCCGGCGA CAACGCCGCC CTGCTGCTCC 500
5 GTGGCCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGATCGT GGCCAAGCCG 550
GGCGCCTACA CGCCGCACAC CGAGTTCGAG GGCTCCGTGT ACATCCTCTC 600
CAAGGACGAG GGTGGCCGCC ACACGCCGTT CTTGACAAC TACCGTCCGC 650
AGTTCTACTT CCGGACGACC GACGTCACCG GCGTCGTCAA GCTGCCGGAG 700
GG 702
10

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2) INFORMATION FOR SEQ ID NO: 35

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium cervicis*
 25 (B) STRAIN: NCTC 10604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35

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GGCTCAGACC CGCGAGCACG TTCTGCTTGC TCGCCAGGTT GCGGTTCCGA 50
30 CGATCCTGGT TGCCCTCAAC AAGGCCGATA TGGTCGACGA TGAGGAAATG 100
CTGGAGCTCG TTGAGGAAGA GTGCCGCGAC CTGCTCGAGT CCCAGGACTT 150
CGATCGTGAC GCCCCGATCA TCCAGGTTTC CGCGCTGAAG GCTCTCGAAG 200
GTGATCCGCA GTGGGTTGCT AAGGTCGAGG AGCTCATGGA GGCAGTCGAC 250
ACCTTCGTGC CGACTCCTGA GCGCGACATG GACAAGCCGT TCCTCATGCC 300
35 GATCGAAGAC GTCTTCACCA TCACCGGCCG TGGCACCGTT GTTACCGGTC 350
GTGTTGAGCG TGGCAAGCTC CCGATCAACT CTGAGGTTGA AATCCTCGGT 400
ATCCGCGAAC CGCAGAAGAC CACCGTTACC GGTATCGAGA TGTTCACAA 450
GTCCATGGAT GAAGCATGGG CAGGCGAGAA CTGTGGTCTC CTCCTGCGTG 500
GCACCAAGCG CGATGAGGTT GAGCGCGGTC AGGTCGTTGC CGTTCCCGGT 550
40 TCGATCACCC CGCACACCAA CTTACCGGA CAGGTCTACA TCCTCAAGAA 600
GGAAGAAGGC GGTTCGTACA ACCCGTTCTT CTCGAACTAC CGTCCGCAGT 650
TCTACTTCCG CACCACGGAC GTGACCGGCG TCATCACCC 689

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45

2) INFORMATION FOR SEQ ID NO: 36

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium flavescens*
 (B) STRAIN: ATCC 10340

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36

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GGTTGTTGCT GCAACCGATG GTCCTATGCC GCAGACCCGC GAGCACGTTC      50
TTCTGGCTCG CCAGGTTGGC GTTCCTTACA TCCTCGTTGC TCTTAACAAG      100
TGCGACATGG TTGATGATGA GGAAATCATC GAGCTCGTTG AGATGGAAAT      150
5 CCGCGAACTG CTCGCTGAGC AGGACTACGA CGAGGATGCC CCCATCATCC      200
ACATCTCCGC TCTCAAGGCT CTTGAGGGTG ACGAGAAGTG GGTACAGGCC      250
ATCGTCGACC TCATGCAGGC CTGCGATGAC TCCATTCCGG ATCCGGAGCG      300
CGAGACCGAC AAGCCCTTCC TCATGCCTAT CGAGGACATC TTCACCATCA      350
CCGGCCGCGG TACCGTTGTT ACCGGCCGTG TTGAGCGTGG CGTTTTGAAG      400
10 GTCAACGAGG ATGTTGAGAT CATCGGCATC AAGGAGAAGT CCATCTCCAC      450
CACCGTTACC GGTATCGAAA TGTTCCGCAA GATGATGGAC TACACCGAGG      500
CTGGCGACAA CTGTGGTCTG CTTCTGCGTG GTACCAAGCG TGAAGAGGTC      550
GAGCGCGGCC AGGTTGTTAT CAAGCCGGGC GCCTACACCC CCCACACCAA      600
GTTTCGAGGGT TCCGTCTACG TCCTCAAGAA GGAAGAGGGC GGCCGCCACA      650
15 CCCC GTTCAT GGACAAC TAC CGTCCG CAGT TCTACT TCCG TACCACTGAC      700
GTGACCGCGG TTGTTACCT GCCTGAGGGC ACCGAGATGG TCATGCCTGG      750
CGACAACGTT GATATGACCG TTGAGCTCAT CCAGCCCGTC GCTAGGATGA      800
GGGC      804

```

20

2) INFORMATION FOR SEQ ID NO: 37

```

(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 692 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

```

(ii) MOLECULE TYPE: Genomic DNA

```

```

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Corynebacterium kutscheri
    (B) STRAIN: ATCC 15677

```

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

```

TGCCTCAGAC CCGTGAGCAC GTTCTTCTTG CTCGCCAGGT TGGCGTTCCCT      50
TACATCCTCG TTGCTCTTAA CAAGTGCGAC ATGGTTGACG ATGAGGAAAT      100
40 CATCGAGCTC GTTGAGATGG AAGTTCGCGA GCTTCTTGCT GAGCAGGAGT      150
ACGATGAAGA GGCTCCAATC ATCCACATCT CTGCTTTGAA GGCTCTTGAG      200
GGCGACGAGA AGTGGACTCA GGCCATCATC GACCTCATGC AGGCTTGTGA      250
TGACTCCATC CCAGATCCAG AGCGTGAGAC CGACAAGCCA TTCCTCATGC      300
CTATCGAGGA TATCTTCACC ATCACC GGTC GTGGCACCGT TGTTACCGGT      350
45 CGTGTGAGC GCGGTTCTT GAAGGTGAAT GAGGACGTCG AGATCATCGG      400
CATCAAGGAG AAGTCCACCA CTACTACCGT TACCGGTATC GAAATGTTCC      450
GTAAGCTTCT TGATTACACC GAAGCTGGCG ATAAGTGTGG TCTGCTTCTT      500
CGTGGTATCA AGCGCGAAGA CGTTGAGCGT GGTCAGGTTG TTGTTAAGCC      550
AGGCGCTTAC ACACCTCACA CCGAGTTCGA GGGCTCTGTT TACGTTCTTT      600
50 CCAAGGACGA GGGCGGCCGC CACACCCCAT TCTTCGACAA CTACCGTCCA      650
CAGTTCTACT TCCGCACCAC TGACGTTACC GGTGTTGTGA AG      692

```

55 2) INFORMATION FOR SEQ ID NO: 38

```

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 797 bases
    (B) TYPE: Nucleic acid
60 (C) STRANDEDNESS: Double

```


(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium minutissimum*

(B) STRAIN: ATCC 23348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38

```

10 CCTGGTTGTT GCTGCAACCG ATGGCCCGAT GCCGCAGACC CGCGAGCACG      50
   TTCTTCTGGC CCGCCAGGTT GGCGTTCGGT ACATCCTCGT TGCACTGAAC      100
   AAGTGTGACA TGGTTGACGA TGAGGAAATC ATCGAGCTCG TTGAGATGGA      150
   GATCCGTGAG CTGCTCGCTG AGCAGGACTA CGACGAGGAA GCTCCGATCG      200
15  TTCACATCTC CGCTCTGAAG GCTCTTGAGG GCGACGAGAA GTGGGCACAG      250
   TCCATCGTTG ACCTGATGCA GGCTTGCGAT GACTCCATCC CGGATCCGGA      300
   GCGCGAGCTG GACAAGCCGT TCCTGATGCC GATCGAGGAC ATCTTCACCA      350
   TTACCGGCCG CGGTACCGTT GTTACCGGCC GTGTTGAGCG TGGCTCCCTG      400
   AACGTTAACG AGGACATCGA GATCATCGGT ATCAAGGACA AGTCCATGTC      450
20  CACCACCGTT ACCGGTATCG AGATGTTCCG CAAGATGATG GACTACACCG      500
   AGGCTGGCGA CAACTGTGGT CTGCTTCTGC GTGGTACCAA GCGTGAAGAG      550
   GTTGAGCGTG GCCAGGTTTG CATCAAGCCG GGCGCTTACA CCCCACACAC      600
   CAAGTTCGAG GGTTCCTGCT ACGTCCTGAA GAAGGAAGAG GGCGGCCCGCC      650
   ACACCCCGTT CATGGACAAC TACCGTCCGC AGTTCTACTT CCGCACCACC      700
25  GACGTCACCG GTGTCATCAA GCTGCCGGAG GGCACCGAGA TGGTCATGCC      750
   GGGCGACAAC GTTGAGATGT CCGTAGAGCT GATCCAGCCG GTCGCTA      797

```

30 2) INFORMATION FOR SEQ ID NO: 39

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 702 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium mycetoides*

(B) STRAIN: ATCC 21134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

```

45 GCCGCAGACC CGCGAGCACG TTCTTCTGGC CCGCCAGGTC GGCGTCCCCT      50
   ACATCCTCGT TGCGCTGAAC AAGTGCGACA TGGTTGATGA TGAGGAGATC      100
   ATCGAGCTCG TGGAGATGGA GGTCCGTGAG CTGCTCGGCG AGCAGGACTA      150
   CGACGAGGAC GCCCCATCA TCCACATCTC CGCTCTGAAG GCTCTCGAGG      200
50  GCGACGAGAA GTGGGTTTCA TCCGTGCTCG ACCTCATGCA GGCGTGCGAC      250
   GACTCCATCC CGGATCCGGT CCGCGAGACC GACCGCGACT TCCTGATGCC      300
   GATCGAGGAC ATCTTCACCA TCTCCGGCCG CGGCACCGTG GTTACCGGTC      350
   GTGTGGAGCG CGGCGTGCTC AACCTCAACG ACGAGGTCGA GATCATCGGC      400
   ATCCGCGACA AGTCCCAGAA GACCACCGTC ACCTCCATCG AGATGTTCAA      450
55  CAAGCTGCTC GATACCGCTG AGGCAGGCCA CAACGCGGCT CTGCTGCTCC      500
   GCGGTCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGGTTGT CATCAAGCCG      550
   GGCGCCTACA CCCCACACAC CAAGTTCGAG GGTTCCTGCT ACCTCCTGTC      600
   CAAGGACGAG GGCGGCCGCC ACACCCCGTT CTTGACAAC TACCGTCCGC      650
   AGTTCTACTT CCGCACCACC GACGTGACCG GTGTTGTGAA GTCGCCGGAG      700
60  GG                                     702

```

2) INFORMATION FOR SEQ ID NO: 40

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudogenitalium*
 (B) STRAIN: ATCC 33038

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40

20	GCTCGCCAGG TTGGCGTTCC TTACATCCTC GTTGGCGCTGA ACAAGTGCGA	50
	CATGGTTGAT GATGAGGAAA TCATCGAGCT CGTTGAGATG GAGATCCGTG	100
	AGCTGCTCGC AGAGCAGGAT TACGATGAGG AAGCTCCTAT CGTTCACATC	150
	TCCGCTCTGA AGGCCCTCGA GGGCGATGAC AAGTGGGTAC AGTCCGTCGT	200
	TGATCTGATG GAAGCCTGCG ACAACTCCAT CCCGGATCCG GAGCGCGCTA	250
25	CCGACCAGCC GTTCCTGATG CCTATCGAGG ACATCTTCAC CATTACCGGC	300
	CGCGGTACCG TTGTTACCGG CCGTGTGAG CGTGGCCGTC TGAACGTCAA	350
	CGAGGACGTT GAGATCATCG GTATCCAGGA GAAGTCCCAG ACCACCACCG	400
	TTACCGGTAT CGAGATGTTT CGCAAGATGA TGGACTACAC CGAGGCTGGC	450
	GACAACTGTG GTCTGCTTCT GCGTGGTACC AAGCGTGAGG ACGTTGAGCG	500
30	TGGCCAGGTT GTTATCAAGC CGGGCGCTTA CACCCCGCAC ACCAAGTTCG	550
	AGGGCTCCGT CTACGTCCTG AAGAAGGAAG AGGGCGGCCG CCACACCCCG	600
	TTCATGAACA ACTACCGTCC GCAGTTCTAC TTCCGTACCA CGGACGTTAC	650
	CGGTGTTGTT CACCTGCCAG AGGG	674

35

2) INFORMATION FOR SEQ ID NO: 41

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium renale*
 (B) STRAIN: ATCC 19412

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41

	TGCCTCAGAC CCGTGAGCAC GTTCTGCTTG CTCGTCAGGT CGGCGTTCCT	50
	TACATCCTCG TTGCACTGAA CAAGTGCAGC ATGGTCGACG ACGAAGAAAT	100
55	CATCGAGCTC GTCGAGATGG AAATCCGTGA ACTGCTCGCA GAGCAGGACT	150
	ACGATGAGGA AGCTCCTATC GTTCACATCT CCGCTCTGGG CGCCCTGAAC	200
	GGCGAGCAGA AGTGGGTTGA CTCCATCGTC GAACTGATGG AAGCTTGCGA	250
	CAACTCCATC CCAGACCCAG TTCGCGACAT CGACCACCCA TTCCTGATGC	300
	CTATCGAGGA CATCTTCACC ATTACCGGTC GCGGTACCGT TGTTACCGGC	350
60	CGTGTGAGC GTGGCCGTCT CAACGTCAAC GAAGAAGTTG AGATCATCGG	400

	TATCAAGGAC	AAGTCCCAGA	AGACCACCGT	CACCGGTATC	GAGATGTTCC	450
	GCAAGATGCT	GGACTACACC	GAAGCTGGCG	ACAACGTGGG	TCTGCTGCTC	500
	CGCGGCATCG	GCCGTGAGGA	TGTCGAGCGT	GGCCAGGTTA	TCATCAAGCC	550
	AGGCGCTTAC	ACCCCTCACT	CTGAGTTCGA	GGGCTCTGTC	TACGTCCTGT	600
5	CCAAGGACGA	GGGTGGCCGC	CACACCCCAT	TCTTCGACAA	CTACCGTCCA	650
	CAGTTCTACT	TCCGCACCAC	CGACGTGACC	GGCGTTGTGC	ACCT	694

10 2) INFORMATION FOR SEQ ID NO: 42

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 687 bases
	(B)	TYPE: Nucleic acid
15	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Corynebacterium ulcerans</i>
	(B)	STRAIN: NCTC 8665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42

25	GCCGCAGACC	CGCGAGCACG	TTCTGCTGGC	TCGCCAGGTT	GGCGTTCCKT	50
	ACATCCTSGT	TGCACTGAAC	AAGTGCGACA	TGGTTGACGA	TGAGGARCTC	100
	CTSGAGCTCG	TCGAGATGGA	GGTCCGCGAG	CTGCTGGCTG	AGCAGGACTA	150
	CGACGAGGAA	GCTCCGRTCG	TTACATCTC	CGCWCTGAAC	GCCCTGGACG	200
30	GCGACSAGAA	GTGGGCTVAC	TCCATCCTCG	AGCTGATGCA	GGCTTGCGAC	250
	GAGTCCATCC	CGGATCCGGA	GCGCGAGACC	GACAAGCCGT	TCCTGATGCC	300
	GATTGAGGAC	ATCTTCACCA	TTACCGGTCTG	CGGYACCGTT	GTTACCGGCC	350
	GTGTTGAGCG	TGGCDTCCTG	AACGTSAAAC	ACGASGTTGA	GATCATGGGY	400
	ATCCGGGAGA	AGTCCCAGAA	GACCACCGTY	ACCKSCATCG	AGATGTTCAA	450
35	CAAGMTGMTG	GACWCCGCAG	AGGCTGGCGA	CAACGCTGSW	CTGCTGCTGC	500
	GTGGTMTSAA	GCGTGAGGAC	GTTGAGCGTG	GCCAGATCAT	CGYTAAGCCG	550
	GGCGCKTACA	CCCCGCACAC	CGAGTTCGAG	GGCTCCGTCT	ACGTCCTGTC	600
	CAAGGACGAG	GGCGGCCGCC	ACACCCCGTT	CTTCGACAAC	TACCGTCCGC	650
40	AGTTCTACTT	CCGCACCACC	GACGTSACCG	GTGTTGT		687

2) INFORMATION FOR SEQ ID NO: 43

45 (i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 778 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
50	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Corynebacterium urealyticum</i>
55	(B)	STRAIN: ATCC 43042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43

	CTGGTTGTTG	CTGCAACCGA	TGGCCCGATG	CCGCAGACCC	GTGAGCACGT	50
60	TCTGCTGGCT	CGCCAGGTTG	GCGTTCCGTA	CATCCTCGTT	GCACTGAACA	100

```

AGTGCGACAT GGTGACGAT GAGGAGCTCC TCGAGCTCGT CGAGATGGAG      150
GTCCGCGAGC TTCTGGCTGA GCAGGACTAC GACGAGGAGG CTCCGGTCGT      200
CCCGATCTCC GCACTGGGCG CCCTGGACGG CGATCAGAAG TGGGTGCGACT      250
CCATCCTCGA GCTCATGAAG GCTTGCGACG AGTCCATCCC GGACCCGGAG      300
5  CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGAGGACA TCTTCACCAT      350
TACCGGTCGC GGCACCGTCG TTACCGGCCG TGTGAGCGT GCGGTCCTGA      400
ACCTGAACGA CGAGGTCGAG ATCCTGGGCA TCCGCGAGAA GTCCACCAAG      450
ACCACCGTCA CCTCCATCGA GATGTTCAAC AAGCTGCTGG ACACCGCAGA      500
GGCTGGCGAC AACGCTGCAC TGCTGCTGCG TGGTCTGAAG CGTGAGGACG      550
10 TCGAGCGAGG CCAGATCATC GCTAAGCCGG GCGCTTACAC CCCGCACACC      600
GAGTTCGAGG GCTCCGTCTA CGTCCTGTCC AAGGACGAGG GCGGCCGTCA      650
CACCCCGTTC TTCGACAAC TCCGTCGCGA GTTCTACTTC CGTACCACCG      700
ACGTCACCGG TGTCGTTACC CTGCCAGAGG GCACCGACAT GGTCATGCCG      750
GGCGACAACG TTGAGATGAG CGTCAAGC      778
15

```

2) INFORMATION FOR SEQ ID NO: 44

```

20  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 703 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
25  (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Corynebacterium xerosis
30  (B) STRAIN: ATCC 373

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44

```

CGCAGACCCG TGAGCACGTC CTCCTGGCCC GCCAGGTCGG CGTCCCCTAC      50
35  ATCCTCGTCG CCCTGAACAA GTGCGACATG GTCGACGATG AGGAGATCAT      100
CGAGCTCGTG GAGATGGAGG TGCGTGAGCT TCTCGCCGAG CAGGACTACG      150
ACGAGGAGGC CCCGATCGTG CACATCTCCG CCCTGGGCGC CCTCAATGGC      200
GAAGAGAAGT GGGTCGACTC CATCGTCGAG CTCATGAACG CCGTCGACGA      250
GAACGTTCCG GACCCGGTCC GCGAGACCGA CAAGCCGTTC CTGATGCCCG      300
40  TCGAGGACAT CTTACCATC ACCGGCCGCG GCACCGTCGC CACCGGTCGC      350
GTGGAGCGCG GCACCCTGAA GGTCAACGAC GAGGTCGAGA TCCTGGGCAT      400
CCAGGAGAAG TCCCAGACCA CCACCGTCAC CGGCATCGAG ATGTTCCGCA      450
AGCTGCTGGA CTCCGCCGAG GCCGGCGACA ACTGTGGCCT GCTGCTCCGC      500
GGCATCAAGC GCGAGGACAT CGAGCGCGGC CAGATCATCG CGAAGCCGGG      550
45  CGCCTACACC CCGCACACCG AGTTCGAGGG CTCCGTCTAC ATCCTGGCCA      600
AGGACGAGGG CGGCCGCCAC ACCCCGTTCT TCGACAAC TA CCGTCCGCAG      650
TTCTACTTCC GCACCACCGA CGTCACCGGC GTCGTGAAGC TGCCGAGGG      700
CAC      703
50

```

2) INFORMATION FOR SEQ ID NO: 45

```

55  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 832 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
60  (ii) MOLECULE TYPE: Genomic DNA

```

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coxiella burnetii*
 (B) STRAIN: Nine Mile phase II

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45

```

GGAGCGATAT TGGTGGTGAG CGCAGCGGAC GGCCCGATGC CGCAAACGCG      50
GGAACACATT GTATTGGCGA AGCAAGTGGG TGTTCCGAAC ATAGTGTTT      100
10 ACTTGAACAA AGCGGACATG GTGGATGACA AAGAGCTGTT GGAATTAGTG      150
GAAATGGAAG TGAGGGATTT ATTGAACAGT TATGATTTC CTGGGGATGA      200
GACGCCGATA ATAGTGGGGT CAGCGTTAAA GCGGTTAGAA GGTGACAAGA      250
GTGAGGTTGG GGAGCCATCG ATAATCAAAT TAGTGGAAAC GATGGACACG      300
TACTTCCCGC AGCCGGAGCG AGCGATAGAC AAACCGTTTT TAATGCCGAT      350
15 CGAAGATGTG TTTTCGATAT CGGGCCGAGG GACGGTGGTG ACGGGACGCG      400
TAGAGCGAGG GATCATCAA GTGGCGGACG AGATAGAGAT TGTGGGGATC      450
AAGGACACGA CGAAGACGAC GTGCACGGGC GTTGAGATGT TTCGCAAATT      500
ATTGGATGAA GGTCAAGCGG GTGACAACGT AGGAATTTTA TTGAGAGGGA      550
CGAAACGCGA AGAAGTGGAG CGTGGTCAAG TATTGGCGAA ACCGGGATCG      600
20 ATCACGCCAC ACAAGAAATT TGAGGCGGAG ATTTATGTGT TGTCGAAGGA      650
AGAAGGGGGA CGCCACACAC CGTTTTTACA AGGCTATCGA CCGCAATTTT      700
ATTTCCGCAC GACGGACGTG ACGGGCCAGT TATTGAGTTT ACCGGAGGGG      750
ATAGAGATGG TGATGCCGGG AGATAACGTG AAAGTGACGG TTGAATTGAT      800
TGCGCCGGTA GCGATGGATG AAGGGCTACG AT      832
25

```

2) INFORMATION FOR SEQ ID NO: 46

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella hoshinae*
 (B) STRAIN: ATCC 33379

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46

```

GGCGCTATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG      50
45 TGAGCACATC CTGCTGGGTC GCCAGGTAGG CGTTCGTAC ATCATCGTGT      100
TCCTGAACAA GTGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT      150
GAGATGGAAG TTCGCGAACT GCTGTCTCAG TACGATTTC CGGGCGACGA      200
TACGCCGGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GGCGAAGCCG      250
AGTGGGAAGC GAAGATCATC GAACTGGCTG AAACGCTGGA CTCCTACATT      300
50 CCGGAACCTG AGCGTGACAT CGACAAGCCG TTCCTGCTGC CGATCGAAGA      350
CGTATTCTCA ATCTCTGCTC GTGGTACCGT TGTACCGGT CGTGTAAGC      400
GCGGTATCAT CAAGGTAGGC GACGAAGTTG AAATCGTAGG TATCAAGCCG      450
ACCACCAAGA CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTACCAAGC      550
55 GTGACGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCACT      600
CCGCACACCA AGTTCGAATC AGAAGTGTAC ATCCTGAGCA AGGATGAAGG      650
CGGCCGTCAT ACTCCGTTCT TCAAAGGTTA CCGTCCGCAG TTCTACTTCC      700
GTACCACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG      750
GTAATGCCGG GCGACAACAT CAAGATGGTT GTTACCCTGA TCCACCCGAT      800
60 CGCCATGGAC GATGGT      816

```

2) INFORMATION FOR SEQ ID NO: 47

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella tarda*
 (B) STRAIN: ATCC 15947

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47

20 GGC GCG ATCC TGG TTG TTG C TGC GACT GAC GGCC CGAT GC CGC AGAC CCG 50
 TGAG CAC ATC CTG TTG GGT C GCC AGG TAGG CGTT CCG TAC ATCAT CGT GT 100
 TCCT GAA CAA GTG CGA CAT G GTT GAT GAC G AAG AGC TGT G GGA ACT GGT T 150
 GAG ATG GAA G TTC GCG AACT GCT GTCT CAG TAC GACT TCC CGG GCG AC GA 200
 CAC GCC GGT A ATCC GCG GTT CTG CGCT GAA AGCG CTG GAA GGCG AAG CCG 250
 25 AGT GGG AAG C GAAG ATCAT C GAA CTGG CTG AA ACTCT GGA CTC CTAC ATC 300
 CCG GAA CCT G AGCG TGAC AT CGACA AGCCG TTC CTG CTGC CGAT CGA AGA 350
 CGT ATT CTCT ATCT CTGG CC GTGG TACC GT TGT TACC GT CGT GTAG AGC 400
 GCG GTAT CAT CAAG GTAG GC GAC GAAG TTG AAAT CGT TGG TAT CAAG CCG 450
 ACC ACCA AGA CCAC CTGT AC TGG CGT TGA ATG TTCC GA AACT GCT GGA 500
 30 CGA AGGCC GT GCT GGT GAG A ACG TTGG TGT TCT GCT GCG GTG TACT AAG C 550
 GTG ACG AAAT CGA ACG TGGT CAG GTACT GG CTA AGCC GGG CAC CAT CACT 600
 CCG CAC ACCA AGT TCG AAT C TGA AGT GTAC ATC CTG AGCA AGG ATGA AGG 650
 CGGCC GTC AT CTCC GTT CT TCA AAG GCTA CCG TCC GCA G TTCT ACT TCC 700
 GTACT ACT GA CTG ACT GGT ACC ATCG AAC TGCC GGA AGG CGT AGAG ATG 750
 35 GTA ATGCC CG GCG ACA ACAT CAAG ATGG TT GTT ACC CTGA TCC ACC CGAT 800
 CGCC ATGG AC GAT GGT CTGC G 821

40 2) INFORMATION FOR SEQ ID NO: 48

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eikenella corrodens*
 (B) STRAIN: ATCC 23834

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48

55

CGGT GCC ATC CTGG TGG TAT CCG CTG CTGA CGG CCCC ATG CCT CAG ACTC 50
 GCG AAC ACAT CCT GTT GGT CTG TCAG G TAG GTGT ACC CTA CAT CCT CGTA 100
 TTC ATG AACA AAT GCG ACAT GGT AGAT GAT GCC GAG CTGC TTG AGT TGGT 150
 TGAG ATG GAA ATCC GCG ACC TGCT CTCC AG CTAT GACT TC CCT GGT GAC G 200
 60 ACT G C CCG AT CGT ACA AGGT TCC GCT CTCA AAG CCT CGA AGG CGAT GCC 250

	GGTTACAAAG	AAAAAATCTT	CGAACTAGCT	GCTGCTTTGG	ATAGCTACAT	300
	CCCCACTCCT	CAACGTGCTG	TAGACAAACC	CTTCCTGTTG	CCGATCGAAG	350
	ACGTATTCTC	TATCTCCGGC	CGTGGTACCG	TAGTAACCGG	TCGTGTAGAG	400
	CGCGGCATCA	TCAAAGTAGG	TGAAGAGATC	GAAATCGTTG	GTCTGAAGCC	450
5	CACTCAGAAA	ACTACCTGTA	CTGGCGTGGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCA	GGCCGGTGAC	AACGTAGGCG	TACTGCTGCG	CGGTACCAAA	550
	CGTGAAGAAG	TTGAGCGTGG	TCAAGTATTG	GCTAAACCCG	GCACCATCAC	600
	TCCGCACACC	AAGTTCAAAG	CCGAAGTATA	CGTATTGAGC	AAAGAAGAAG	650
	GTGGTCGTCA	CACCCCGTTC	TTTGCCAAC	ACCGTCCACA	GTTCTACTTC	700
10	CGTACTACTG	ACGTAACCGG	TGCTGTAGAG	CTGGAGCCTG	GTGTAGAAAT	750
	GGTTATGCCT	GGTGAGAACG	TAACCATCAC	CGTAGAACTG	ATTGCTCCGA	800
	TTGCTATGGA	AGAAGGTCTG	CGCTTTGCGA			830

15

2) INFORMATION FOR SEQ ID NO: 49

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 808 bases
20	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Enterobacter aerogenes</i>
	(B)	STRAIN: ATCC 13048

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49

	GGCGCGATCC	TGTTTGTGTC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
35	GAGATGGAAG	TTCGTGAACT	GCTGTCTCAG	TACGATTTCC	CGGGCGACGA	200
	CACTCCGATC	GTTCTGTGGT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	250
	AGTGGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATC	300
	CCGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
40	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGCGAAAA	CCACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGYGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CAGCATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGATC	ATCCTGTCCA	AAGACGAAGG	650
45	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACTGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGRTG	750
	GTAATGCCCG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCGATGG					808

50

2) INFORMATION FOR SEQ ID NO: 50

(i) SEQUENCE CHARACTERISTICS:

55	(A)	LENGTH: 828 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter agglomerans*
 (B) STRAIN: ATCC 27989

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
10	TTCCTGAACA	AATGTGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ATACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAMGCW	250
	GAGTGGGAAG	CGAAAATCAT	CGARCTGGCT	GGCCACCTGG	ATACCTATAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATCTCCGGT	CGCGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TYAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	TACYGCGAAA	TCAACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
20	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGTCGTCA	CACTCCGTTT	TTCAAAGGCT	ACCGTCCSCA	GTTCTACTTC	700
	CGTACAACTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
25	TCGCGATGGA	CGACGGTCTG	CGTTCGCA			828

2) INFORMATION FOR SEQ ID NO: 51

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter amnigenus*
 (B) STRAIN: ATCC 33072

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51

	TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACGC	50
45	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCAGGTGATG	200
	ACACTCCAAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAAGCA	250
	GAGTGGGAAG	CTAAAATCGT	TGAGCTGGCT	GGCTACCTGG	ATTCTTACAT	300
50	CCCGGAACCA	GAACGTGCTA	TCGATAAGCC	ATTCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	TATCTCCGGC	CGTGGTACTG	TTGTAACCGG	TCGTGTAGAG	400
	CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCTAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
55	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCAG	GCTCAATCAA	600
	GCCGCACACC	AAATTCGAAT	CTGAAGTTTA	TATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACTG	ACGTGACCGG	CACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGCGACAACA	TTCAGATGGT	TGTTACCCTG	ATCCACCCAA	800
60	TCGCGATGGA	TGACGGTCTG	CGTTT			825

2) INFORMATION FOR SEQ ID NO: 52

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter asburiae*
 (B) STRAIN: ATCC 35953

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52

20	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTT	CATCATCGTG	100
	TTCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAGATGGAA	GTTTCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ATACTCCAAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
25	GAGTGGGAAG	CGAAAATCAT	CGAAGTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCGA	TTGACAAAGCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCTAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
30	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCGAAGCCAG	GCTCAATCAA	600
	GCCACACACC	AAGTTCGAAT	CTGAAAGTGA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTTGAGAT	750
35	GGTAATGCCA	GCGGACAACA	TCAAGATGGT	TGTGACTCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGTCTG	CG			822

40 2) INFORMATION FOR SEQ ID NO: 53

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cancerogenus*
 (B) STRAIN: ATCC 35317

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53

55

55	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
	TTCTGAACA	AGTGCACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTTCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCAGGCGACG	200
60	ACACTCCAAT	CGTTCGTGGT	TCCGCGCTGA	AAGCGCTGGA	AGGCGAAGCT	250

	GAGTGGGAAG	CAAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCGA	TTGACAAGCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
5	TACTGCKAAA	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGCGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCGAAGCCAG	GCTCAATCAA	600
	GCCACACACC	AAGTTCGAAT	CTGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
10	CGTACAACTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGCGACAACA	TCAAGATGGT	TGTGACGCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

15

2) INFORMATION FOR SEQ ID NO: 54

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 806 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter cloacae*

(B) STRAIN: ATCC 13047

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54

	GATCCTGGTA	GTAGCTGCGA	CTGACGGCCC	AATGCCTCAG	ACTCGTGAGC	50
	ACATCCTGCT	GGGTCGTCAG	GTAGGCGTTC	CTTACATCAT	CGTGTTCTCTG	100
	AACAAATGCG	ACATGGTTGA	TGACGAAGAG	CTGCTGGAAC	TGGTAGAGAT	150
35	GGAAGTTCGT	GAAGTCTGT	CTCAGTACGA	TTTCCCAGGC	GACGATACCC	200
	CAATCGTTCG	TGGTTCCTGCT	CTGAAAGCGC	TGGAAGGCGA	CGCAGAGTGG	250
	GAAGMGAAAA	TCATCGAACT	GGCTGGCTAC	CTGGATTCTT	ACATCCCAGA	300
	ACCAGAGCGT	GCGATTGAYA	AGCCATTCTT	GCTGCCAATC	GAAGACGTAT	350
	TCTCCATCTC	CGGTCGTGGT	ACCGTTGTTA	CCGGTCGTGT	AGAGCGCGGT	400
40	ATCATCAAG	TGGGTGAAGA	AGTTGAAATC	GTTGGTATCA	AAGAGACTGC	450
	GAAGTCTACC	TGACTGGCG	TTGAAATGTT	CCGCAAACTG	CTGGACGAAG	500
	GCCGTGCTGG	TGAGAACGTT	GGTGTCTGCT	TGCGTGGTAT	CAAACGTGAA	550
	GAAATCGAAC	GTGGTCAGGT	TCTGGCGAAG	CCAGGCTCAA	TCAAGCCACA	600
	CACCAAGTTC	GAATCTGAAG	TGTACATCCT	GTCCAAAGAC	GAAGGCGGCC	650
45	GTCATACTCC	GTTCTTCAAA	GGCTACCGTC	CACAGTTCTA	CTTCCGTACA	700
	ACTGACGTGA	CCGGTACCAT	CGAACTGCCA	GAAGGCGTAG	AGGTGGTAAT	750
	GCCAGGCGAC	AACATCAAGA	TGGTTGTGAC	TCTGATCCAC	CCAATCGCGA	800
	TGGACG					806

50

2) INFORMATION FOR SEQ ID NO: 55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter gergoviae*
 (B) STRAIN: ATCC 33028

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
10	TTCCTGAACA	AGTGCACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAGATGGAA	GTTCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ACACCCCGAT	CGTTCGCGGT	TCTGCGCTGA	AAGCGCTGGA	AGGCGACGCA	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCCACCTGG	ATACCTAYAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCCCTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATTTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAGGTTGG	TGAAGAAATT	GAAATCGTTG	GTATCAAAGA	450
	CACCGCGAAA	ACCACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTCGGCG	TTCTGCTGCG	TGGTATCAAG	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCCG	GCTCCATCAA	600
20	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	CACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAACTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GCGGACAACA	TCAAGATGGT	TGTTACCCTG	ATCCACCCGA	800
25	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

2) INFORMATION FOR SEQ ID NO: 56

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter hormaechei*
 (B) STRAIN: ATCC 49162

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCTATGC	CTCAGACCCG	50
45	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCTTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAGATGGAAG	TTCGTGAACT	GCTGTCTCAG	TACGATTTC	CAGGCGACGA	200
	CACCCCAATC	GTTTCGTGGT	CCGCGCTGAA	AGCGCTGGAA	GGCGAMGCAG	250
	AGTGGGAAGM	GAAAATCATC	GARCTGGCTG	GCTTCCTGGA	TTCTTACATC	300
50	CCAGAACCAG	AGCGTGCGAT	TGACAAGCCA	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTWAGC	400
	GCGGTATCAT	CAAAGTAGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
55	GTGAAGAAAT	CGAACGTGGT	CAGGTTCTGG	CGAAGCCAGG	CTCAATCAAG	600
	CCACACACCA	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGACAACAT	CAAGATGGTT	GTGACGCTGA	TCCACCCCAAT	800
60	CGCGATGGAC	GACGGTCTGC	GTTTCGCAA			829

35

2) INFORMATION FOR SEQ ID NO: 57

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter sakazakii*
 (B) STRAIN: ATCC 29544

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57

20	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
	GAGATGGAAG	TGCGCGAGCT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACCCCGATC	GTTTCGTGGT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCTG	250
25	AGTGGGAAGC	GAAAATCATC	GAGCTGGCAG	GTCACCTGGA	TTCCTACATC	300
	CCGGAACCGG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCYGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAGGTTGGT	GAAGAAGTTG	AAATCGTGGG	CATCAAAGAC	450
	ACCGCGAAAT	CCACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
30	CGAAGGCCGT	GCGGGCGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCCATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	650
	CGGCCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACRGTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTTGAGATG	750
35	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCGATGGAC	GACGGTCTGC	GTTTCGCAAT	C		831

40 2) INFORMATION FOR SEQ ID NO: 58

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58

55

55	CGGCGCGATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACAC	50
	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	GTGTACCATA	CATCGTTGTT	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTGTTCAG	ATATGACTTC	CCAGGCGACG	200
60	ATGTTCTCTG	AATCGCTGGT	TCTGCTTTGA	AAGTCYTGA	AGGCGATGCT	250

	TCATACGAAG	AAAAAATCAT	GGAATTAATG	GCTGCAGTTG	ACGAATACGT	300
	TCCAACTCCA	GAACGTGACA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTGCTGA	450
5	AGAACTGCT	AAAACAACCTG	TAACCTGGTGT	TGAAATGTTC	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGTGT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAG	CTGGTACAAT	600
	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	TTACGTTTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCACACACCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
10	TTCCGTACAA	CTGACGTAAC	TGGTGTGTT	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTAACAAT	CGACGTTGAA	TTGATCCACC	800
	CAATCGCTAT	CGAAGACGGA	ACTCGTTTCT	CAATT		835

15

2) INFORMATION FOR SEQ ID NO: 59

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 826 bases
20	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Enterococcus cecorum</i>
	(B)	STRAIN: ATCC 43198

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59

	GGTGCTATCT	TAGTAGTATC	TGCTGCTGAT	GGTCCTATGC	CACAAACTCG	50
	TGAACACATT	CTTTTATCAC	GTAACGTTGG	TGTTCCATAC	ATCGTTGTTT	100
	TCTTAAACAA	AGTTGATATG	GTTGACGACG	AAGAATTATT	AGAATTAGTT	150
35	GAAATGGAAG	TACGTGACTT	ATTAAC TGAA	TACGACTTCC	CAGGAGACGA	200
	TGTTCTGTGA	ATCGCTGGTT	CTGCATTAAA	AGCTTTAGAA	GGCGACCCAT	250
	CTTACGAAGA	AAAAATCTTA	GAATTAATGG	CTGCAGTTGA	CGAATACATC	300
	CCAAC TCCAG	AACGTGACAA	CGATAAACCA	TTCATGATGC	CAGTCGAAGA	350
	CGTATTTTCA	ATCACTGGTC	GTGGTACTGT	TGCTACAGGT	CGTGTTGAAC	400
40	GTGGACAAGT	ACGTGTTGGT	GACGAAGTTG	AAATAGTTGG	TATCCATGAT	450
	GAAATTTCTA	AAACAACAGT	TACTGGTGTT	GAAATGTTCC	GTAAATTATT	500
	AGATTACGCT	GAAGCTGGAG	ACAACATCGG	TGCATTATTA	CGTGGTGTGG	550
	CTCGTGAAGA	TATCCAACGT	GGTCAAGTAT	TAGCTAAACC	AGGTTCAATC	600
	ACTCCACATA	CAAAATTCAC	TGCTGAAGTG	TACGTTTTAA	CTAAAGAAGA	650
45	AGGTGGACGT	CATACTCCAT	TCTTCACTAA	CTACCGTCCA	CAATTCTACT	700
	TCCGTACAAC	TGACGTTACA	GGTGTAGTTA	ACTTACCAGA	AGGTACTGAA	750
	ATGGTTATGC	CTGGTGATAA	CGTAACTATG	GAAGTTGAAT	TAATCCACCC	800
	AATCGCTATC	GAAGACGGAA	CTCGTT			826

50

2) INFORMATION FOR SEQ ID NO: 60

(i) SEQUENCE CHARACTERISTICS:

55	(A)	LENGTH: 835 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*
 (B) STRAIN: ATCC 51266

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60

	CGGCGCGATC	TTGGTAGTAT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CCTATTGTCA	CGTAACGTTG	GTGTTCCCTTA	CATCGTCGTT	100
10	TTCTTGAACA	AAATGGACAT	GGTTGATGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTGTCAGA	ATACGACTTC	CCAGGCGACG	200
	ACACTCCAGT	TATCGCAGGT	TCAGCTTTGA	AAGCCTTAGA	AGGCGACGCT	250
	TCATATGAAG	AAAAAATCTT	AGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GTTTCGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
15	ATGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCAACTGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTAG	GTATCGCTGA	450
	AGAAACTGCT	AAAACACTG	TAACAGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TGGATTACGC	TGAAGCTGGC	GACAACATTG	GTGCATTATT	ACGTGGTGTG	550
	GCTCGTGAAG	ATATCCAACG	TGGTCAAGTA	TTATCAAAAC	CAGGTTCAAT	600
20	CACTCCACAT	ACAAAATTG	CGGCAGAAGT	TTACGTTTTA	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGCCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACGTTACTAT	GGACGTTGAA	TTAATCCACC	800
25	CAATCGCGAT	CGAAGACGGT	ACTCGTTTCT	CAATC		835

2) INFORMATION FOR SEQ ID NO: 61

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus durans*
 (B) STRAIN: ATCC 19432

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61

	CGGAGCTATC	TTAGTAGTTT	CTGCTGCTGA	TGGCCCTATG	CCTCAAACCTC	50
45	GTGAACATAT	CCTATTATCT	CGTCAAGTTG	GTGTTCCCTTA	CATCGTYGTA	100
	TTCTTGAACA	AAGTAGATAT	GGTCGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTAACAGA	ATACGAATTC	CCTGGTGACG	200
	ATGTTCCCTGT	AATCGCTGGT	TCAGCTTTGA	AAGCTTTAGA	AGGCGACGCT	250
	TCATACGAAG	AAAAAATCCT	TGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
50	CCCAACTCCA	GAACGTGACA	ACGACAAACC	ATTCATGATG	CCAGTTGAAG	350
	ATGTATTCTC	RATCACTGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGTTGTA	GATATCGTTG	GTATCGCAGA	450
	AGAAACAGCT	CAAACAACAG	TTACTGGTGT	TGAAATGTTT	CGTAAATTAT	500
	TAGRCTACGC	TGAAGCTGGA	GACAACATTG	GTGCTTTACT	ACGTGGTGTG	550
55	GCACGTGAAG	ACATCCAACG	TGGACAAGTT	TTAGCTAAAC	CAGGTACAAT	600
	CACKCCTCAT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGCGACA	ACGTAACAAT	GGAAGTTGAA	TTAATCCACC	800
60	CAATCGCTAT	CGAAAATGGT	ACTAAATTCT	CAATC		835

2) INFORMATION FOR SEQ ID NO: 62

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R610

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62

20	AGTAGTTTCT	GCTGCTGATG	GTCCTATGCC	TCAAACACGT	GAACATATCT	50
	TATTATCACG	TAACGTTGGT	GTACCATACA	TCGTTGTATT	CTTAAACAAA	100
	ATGGATATGG	TTGATGACGA	AGAATTATTA	GAATTAGTAG	AAATGGAAGT	150
	TCGTGACTTA	TTATCAGAAT	ACGATTTCCT	AGGCGATGAT	GTTCCAGTTA	200
	TCGCAGGTTT	TGCTTTGAAA	GCTTTAGAAG	GCGACGAGTC	TTATGAAGAA	250
25	AAAATCTTAG	AATTAATGGC	TGCAGTTGAC	GAATATATCC	CAACTCCAGA	300
	ACGTGATACT	GACAAACCAT	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	350
	TCACTGGACG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	TGGTGAAGTT	400
	CGCGTTGGTG	ACGAAGTTGA	AATCGTTGGT	ATTAAAGACG	AAACATCTAA	450
	AACAACGTGT	ACAGGTGTTG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	500
30	AAGCAGGCGA	CAACATCGGT	GCTTTATTAC	GTGGTGTAGC	ACGTGAAGAT	550
	ATCGAACGTG	GACAAGTATT	AGCTAAACCA	GCTACAATCA	CTCCACACAC	600
	AAAATTCAAA	GCTGAAGTAT	ACGTATTATC	AAAAGAAGAA	GGCGGACGTC	650
	ACACTCCATT	CTTCACTAAC	TACCGTCCTC			680

35

2) INFORMATION FOR SEQ ID NO: 63

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R487

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63

	AGTAGTTTCT	GCTGCTGATG	GTCCTATGCC	TCAAACACGT	GAACATATCT	50
	TATTATCACG	TAACGTTGGT	GTACCATACA	TCGTTGTATT	CTTAAACAAA	100
55	ATGGATATGG	TTGATGACGA	AGAATTATTA	GAATTAGTAG	AAATGGAAGT	150
	TCGTGACTTA	TTATCAGAAT	ACGATTTCCT	AGGCGATGAT	GTTCCAGTTA	200
	TCGCAGGTTT	TGCTTTGAAA	GCTTTAGAAG	GCGACGAGTC	TTATGAAGAA	250
	AAAATCTTAG	AATTAATGGC	TGCAGTTGAC	GAATATATCC	CAACTCCAGA	300
	ACGTGATACT	GACAAACCAT	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	350
60	TCACTGGACG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	TGGTGAAGTT	400

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CGCGTTGGTG ACGAAGTTGA AATCGTTGGT ATTAAAGACG AAACATCTAA      450
AACAACTGTT ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG      500
AAGCAGGCGA CAACATCGGT GCTTTATTAC GTGGTGTAGC ACGTGAAGAT      550
ATCGAACGTG GACAAGTATT AGCTAAACCA GCTACAATCA CTCCACACAC      600
5 AAAATTCAAA GCTGAAGTAT ACGTATTATC AAAAGAAGAA GCGGACGTC      650
ACACTCCATT CTTACTAAC TACCGTCCTC      680

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10 2) INFORMATION FOR SEQ ID NO: 64

(i) SEQUENCE CHARACTERISTICS:

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15 (A) LENGTH: 685 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Enterococcus faecium
    (B) STRAIN: R482

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64

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25 AGTAGTTTCT GCTGCTGACG GCCCAATGCC TCAAACTCGT GAACACATCC      50
   TATTGTCTCG TCAAGTTGGT GTTCCTTACA TCGTTGTATT CTTGAACAAA      100
   GTAGACATGG TTGATGACGA AGAATTACTA GAATTAGTTG AAATGGAAGT      150
   TCGTGACCTA TTAACAGAAT ACGAATTCCC TGGTGACGAT GTTCCTGTAG      200
30 TTGCTGGATC AGCTTTGAAA GCTCTAGAAG GCGACGCTTC ATACGAAGAA      250
   AAAATTCTTG AATTAATGGC TGCAGTTGAC GAATACATCC CAACTCCAGA      300
   ACGTGACAAC GACAAACCAT TCATGATGCC AGTTGAAGAC GTGTTCTCAA      350
   TTAGTGGACG TGGTACTGTT GCTACAGGTC GTGTTGAACG TGGACAAGTT      400
   CGCGTTGGTG ACGAAGTTGA AGTTGTTGGT ATTGCTGAAG AAACCTCAAA      450
35 AACAACAGTT ACTGGTGTG AAATGTTCCG TAAATTGTTA GACTACGCTG      500
   AAGCTGGAGA CAACATTGGT GCTTTACTAC GTGGTGTGTC ACGTGAAGAC      550
   ATCCAACGTG GACAAGTTT AGCTAAACCA GGTACAATCA CACCTCATAC      600
   AAAATTCTCT GCAGAAGTAT ACGTGTTGAC AAAAGAAGAA GGTGGACGTC      650
40 ATACTCCATT CTTACTAAC TACCGTCCTC AATTT      685

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2) INFORMATION FOR SEQ ID NO: 65

45 (i) SEQUENCE CHARACTERISTICS:

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    (A) LENGTH: 825 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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55 (A) ORGANISM: Enterococcus flavescens
    (B) STRAIN: ATCC 49996

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65

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60 CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTAYG CCTCAAACAC      50
   GTGAACACAT CTTGTTATCA CGTAACGTTG GTGTACCATA CATCGTTGTT      100

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	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTGTCTAGA	ATATGACTTC	CCAGGCGACG	200
	ATGTTCTCTGT	AATCGCTGGT	TCTGCTTTGA	AAGCTCTTGA	AGGCGATGCT	250
	TCATACGAAG	AAAAAATCAT	GGAATTAATG	GCTGCAGTTG	ACGAATACGT	300
5	TCCAACCTCCA	GAACGTGACA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTGCTGA	450
	AGAAACTGCT	AAAACAACTG	TAAC TGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGGGTT	550
10	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTAGCTAAAG	CTGGTACAAT	600
	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	TTACGTTTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCTACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTT	GAATTACCAG	AAGGAAC TGA	750
	AATGGTTATG	CCTGGTGATA	AMGTAACAAT	CGACGTTGAA	TTGATCCACC	800
15	CAATCGCTAT	CGAAGACGGA	ACTCG			825

2) INFORMATION FOR SEQ ID NO: 66

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Enterococcus gallinarum*
- (B) STRAIN: R420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66

35	TCCTATGCCT	CAAAC TCGTG	AACACATCTT	GTTATCACGT	AACGTTGGCG	50
	TACCATA CAT	CGTTGTTTTT	TTGAACAAAA	TGGATATGGT	TGATGACGAA	100
	GAATTGCTAG	AATTAGTTGA	AATGGAAGTT	CGTGACCTAT	TGTCTGAGTA	150
	TGACTTCCCA	GGCGACGATG	TTCTGTAAAT	CGCCGGTTCT	GCTTTGAAAG	200
	CTCTTGAAGG	AGATCCTTCA	TACGAAGAAA	AAATCATGGA	ATTGATGGCT	250
40	GCAGTTGACG	AATACGTTCC	AACTCCAGAA	CGTGATACTG	ACAAACCATT	300
	CATGATGCCA	GTCGAAGACG	TATTCTCAAT	CACTGGACGT	GGTACTGTTG	350
	CTACAGGCCG	TGTTGAACGT	GGACAAGTTC	GCGTTGGTGA	TGAAGTAGAA	400
	ATCGTTGGTA	TTGCTGACGA	AACTGCTAAA	ACAACTGTAA	CAGGTGTTGA	450
	AATGTTCCGT	AAATTGTTAG	ACTATGCTGA	AGCAGGGGAT	AACATTGGTG	500
45	CATTGCTACG	TGGGGTTGCT	CGTGAAGACA	TCCAACGTGG	ACAAGTATTG	550
	GCTAAAGCTG	GTACAATCAC	ACCTCATACA	AAATTCAAAG	CTGAAGTTTA	600
	TGTTTTGACA	AAAGAAGAAG	GTGGACGTCA	CACTCC		636

50

2) INFORMATION FOR SEQ ID NO: 67

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 835 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus hirae*

(B) STRAIN: ATCC 8043

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67

	CGGAGCTATC	TTAGTAGTTT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACCTC	50
	GTGAACATAT	CCTAYTATCT	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCTTGAACA	AAGTAGATAT	GGTTGACGAC	GAAGAATTAC	TAGAATTAGT	150
10	TGAAATGGAA	GTTTCGTGACT	TATTAACAGA	ATACGAATTC	CCTGGTGACG	200
	ATGTTTCCTGT	AGTTGCTGGT	YCAGCTTTGA	AAGCTTTAGA	AGGCGACGCT	250
	TCATACGAAG	AAAAAATCCT	TGAATTGATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGACA	ACGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
15	CGTGGACAAG	TTCGCGTTGG	TGACGTTGTA	GATATCGTTG	GTATCGCAGA	450
	AGAAACAGCT	CAAACAACAG	TTACTGGTGT	TGAAATGTTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGA	GACAACATTG	GTGCTTTACT	ACGTGGTGTG	550
	GCACGTGAAG	ACATCCAACG	TGGACAAGTT	TTAGCTAAAC	CAGGTACAAT	600
	CACACCTCAT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACAAAAGAAG	650
20	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACRA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGCGACA	ACGTAACAAT	GGAAGTTGAA	TTAATCCACC	800
	CAATCGCTAT	CGAAAACGGT	ACTAAATTCT	CAATC		835

25

2) INFORMATION FOR SEQ ID NO: 68

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus mundtii*

(B) STRAIN: ATCC 43186

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68

	CGGAGCAATC	TTAGTTGTTT	CTGCTGCTGA	CGGCCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CCTATTATCT	CGTCAAGTTG	GTGTACCATA	CATCGTTGTA	100
45	TTCTTGAACA	AAGTAGATAT	GGTTGATGAC	GAAGAATTAC	TTGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACC	TATTAACAGA	ATACGAATTC	CCTGGTGACG	200
	ATGTTTCCTGT	AATCGCTGGT	TCAGCTTTAA	GAGCTTTAGA	AGGCGACGCT	250
	KCATACGAAG	AAAAAATTCT	TGAATTGATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGATA	ACGACAAACC	ATTCATGATG	CCAGTTGAGG	350
50	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	ACGTGTTGAA	400
	CGTGGACAAG	YTCGTGTTGG	TGACGTTATC	GATATCGTTG	GTATCGCAGA	450
	AGAAACAGCT	CAAACAAGTG	TAACTGGTGT	TGAAATGTTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCAGGC	GATAACATTG	TGCGTTACT	ACGTGGTGTG	550
	TCACGTGAAG	ACATCCAACG	TGGTCAAGTT	TTAGCTAAAC	CAGGTACAAT	600
55	CACACCTCAT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTCYGTACGA	CTGACGTAAC	TRGTGTTGTY	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGCGACA	ACGTAACAAT	GGAAGTTGAA	TTAATCCACC	800
60	CAATCGCTAT	CGAAAATGGT	ACTAAATTCT	CAATC		835

2) INFORMATION FOR SEQ ID NO: 69

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus pseudoavium*
 (B) STRAIN: ATCC 49372

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69

	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCTATG	CCTCAAACAC	50
20	GTGAACACAT	CTTGTTATCT	CGTAACGTTG	GTGTTTCCTTA	CATCGYTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTGTCAGA	ATACGATTTC	CCAGGCGACG	200
	ACACTCYAGT	TATCGCTGGT	TCAGCYTTGA	AAGCTTTAGA	AGGCGACCCCT	250
	TCATACRAAG	AAAAAATCTT	AGAATTAATG	SCTGCTGTTG	ACGAATACAT	300
25	CCCAACACCA	GTTTCGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCAACTGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTAG	GTATCGCTGA	450
	AGAAACTGCT	AAAACAACCTG	TTACAGGTGT	TGAAATGTTC	CGTAAATTGT	500
	TAGACTACGC	TGAAGCAGGC	GATAACATCG	GTGCATTATT	ACGTGGTGTT	550
30	GCACGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAC	CAGCTTCAAT	600
	CACTCCACAT	ACAAAATTCT	CTGCAGAAGT	TTACGTTTTA	ACTAAAGAAG	650
	AAGGCGGGCG	TCACACTCCG	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTGT	GATCTACCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACCTAT	GGAAGTTGAA	TTAATCCACC	800
35	CAATCGCGAT	CGAAGACGGA	ACTCGTTTCT	CTATTC		836

2) INFORMATION FOR SEQ ID NO: 70

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus raffinosus*
 (B) STRAIN: ATCC 49427

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70

55	CGGAGCTRTC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTGTTATCT	CGTAACGTTG	GTGTTTCCTTA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTAACCTGA	ATACGACTTC	CCAGGCGACG	200
	ACACTCCAGT	TATCGCAGGT	TCAGCTTTGA	AAGCCTTAGA	AGGCGACGCT	250
60	TCATACGAAG	AAAAAATCTT	AGAATTAATG	GCTGCTGTTG	ATGAATACAT	300

	CCCAACACCA	GTTCGTGATA	CTGACAAACC	ATTCATGATG	CCAGYGGAAG	350
	ACGTAYTCTC	AATCACTGGT	CGTGGAAGTG	TTGCAACTGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTAG	GTATTGCTGA	450
	AGAAACTGCT	AAAACAACCTG	TTACAGGTGT	TGAAATGTTC	CGTAAATTGT	500
5	TGGATTACGC	TGAAGCGGGC	GACAACATTG	GTGCATTATT	ACGTGGTGT	550
	GCACGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAC	CAGCTTCAAT	600
	CACTCCACAT	ACAAAATTCT	CTGCAGAACT	TTACGTTT	ACTAAAGAAG	650
	AAGGCGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTAGTT	GATCTACCAG	AAGGTACTGA	750
10	AATGGTAATG	CCTGGTGATA	ACGTAACAT	GGAAGTTGAA	TTAATCCACC	800
	CAATCGCGAT	CGAAGACGGA	ACTCGTTTCT	CTATT		835

15 2) INFORMATION FOR SEQ ID NO: 71

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus saccharolyticus*
 (B) STRAIN: ATCC 43076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71

30	CGGCGCGATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTGTTATCT	CGTAACGTAG	GTGTTCCCTTA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCGTGACT	TATTATCAGA	ATACGATTTC	CCAGGCGATG	200
35	ACACTCCAGT	TATTGCAGGT	TCTGCTTTGA	AAGCTTTAGA	AGGCGATCCA	250
	GTTTACGAAG	AAAAAATCTT	CGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGATA	CTGAAAAACC	ATTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGTTGTA	GAAATCGTTG	GTATCGACGA	450
40	AGAAACAGCT	CAAACTACTG	TAACAGGTGT	TGAAATGTTC	CGTAAATTAT	500
	TAGACTACGC	TGAAGCAGGC	GATAACATCG	GTGCTTTATT	ACGTGGGGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTAGCTAAAC	CAGGAACAAT	600
	CACTCCTCAT	ACAAAATTCG	TAGCTGAAGT	TTACGTTT	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	TCAATTCTAC	700
45	TTCCGTACAA	CTGACGTAAC	TGGTGTGTA	GAATTACGCG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGACA	ACGTAACAT	CGACGTTGAA	TTAATCCACC	800
	CAATCGCTAT	CGAAGACGGA	ACTCGTTTCT	CTATT		835

50

2) INFORMATION FOR SEQ ID NO: 72

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus solitarius*

(B) STRAIN: ATCC 49428

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72

	GAGCTATCTT	GGTAGTTTCT	GCAGCTGATG	GCCCAATGCC	ACAAACTCGT	50
	GAACATATTT	TGTTGTCACG	TAATGTAGGT	GTACCTTACA	TCGTTGTGTT	100
	CTTGAACAAA	ATGGATATGG	TTGATGACGA	AGAATTACTT	GAGTTAGTTG	150
10	AAATGGAAGT	ACGTGATCTA	TTATCTGAAT	ACGACTTCCC	AGGAGATGAT	200
	ACTCCAGTTA	TTTCCGGTTC	AGCTTTGAAA	GCTTTAGAAG	GCGACGAAGA	250
	ATATGAACAA	AAAATTATGG	ACTTAATGGA	TGCAGTTGAT	GACTACATTC	300
	CAACTCCTGA	ACGTGACCAT	GACAAACCAT	TCATGATGCC	AATTGAAGAT	350
	GTATTTTCAA	TTACAGGCCG	TGGTACTGTT	GCTACAGGAC	GTGTTGAACG	400
15	CGGGACTATC	AAAGTCGGCG	ATGAAGTTGA	CATTATTGGT	ATTCATGAAG	450
	ACGTTAAAAA	GACAACAGTT	ACTGGTGTAG	AAATGTTCCG	TAAATTGTTG	500
	GACTACGCTG	AAGCAGGCGA	TAACATTGGT	ACTTTGTTAC	GTGGTGTTC	550
	TCGTGATGAT	ATCGAACGTG	GTCAAGTATT	AGCTAAACCA	GGTTCAATCA	600
	CACCACATAC	AAGATTCTCT	GCTGAAGTTT	ATGTTTTGAC	TAAAGAAGAA	650
20	GGCGGACGTC	ATACTCCATT	CTTCTCAAAC	TATCGTCCTC	AATTCTACTT	700
	CCGTACAAC	GATATCACTG	GTGTCATTGA	ATTGCCAGAA	GGTACTGAAA	750
	TGGTAATGCC	AGGTGATAAT	GTAACAATGG	ATGTTGAATT	AATCCACCCA	800
	GTCGCTATCG	AAGAAGGAAC	TCG			823

25

2) INFORMATION FOR SEQ ID NO: 73

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: ATCC 25788

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73

	CGGTGCAATC	TTGGTCGTAT	CAGCGACAGA	TGGCCCAATG	CCACAAACAC	50
	GGGAGCATAT	TTTGCTTTCT	CGTCAAGTGG	GTGTGAAACA	TTTGATCGTC	100
45	TTTTTGAATA	AGACGGACCT	TGTCGATGAT	GACGAGTTGA	TCGATTTAGT	150
	TGAAATGGAA	GTCAGAGAAT	TGCTGACTGA	ATATGATTTT	CCTGGCGACG	200
	ACATTCCTGT	GATCAAGGGC	TCTGCGTTAA	AAGCCTTGGG	AGGGGACCCA	250
	GATGCTGAAG	CAGCGATCTT	AACGCTGATG	GATACAGTAG	ATGAATATAT	300
	CCCAACGCCA	GAACGTGATA	CTGACAAACC	ATTGTTGTTA	CCGATCGAAG	350
50	ATGTCTTTTC	GATCACAGGA	CGGGGGACCG	TTGCTTCTGG	TCGGATCGAT	400
	CGCGGCATGG	TAAAAGTCGG	GGATGAAGTA	GAAATCGTCG	GAATCAAACC	450
	TGAAACACAA	AAAGCAGTCG	TGACAGGGGT	AGAAATGTTT	CGCAAAACGA	500
	TGGACTTCGG	AGAAGCTGGC	GATAACGTAG	GGGTATTGTT	ACGGGGCATC	550
	ACCCGTGATG	AAATTGAACG	TGGCCAAGTG	TTAGCAAAAC	CAGGTTCTAT	600
55	CACACCGCAT	ACGAAATTCC	AAGCGGAAGT	CTATGTGTTG	ACAAAAGAAG	650
	AAGGCGGTCG	CCATACCCCA	TTCTTTAATA	ATTATCGCCC	ACAATTTTAC	700
	TTCCGTACAA	CGGACGTAAC	TGGGAATATC	GTTTTACCAG	AAGGAACGGA	750
	AATGGTGATG	CCTGGTGACA	ACGTAACGAT	CGATGTGGAA	TTGATCCATC	800
60	CGATCGCTGT	AGAAAATGGA	ACGACCTTCT	CGATT		835

2) INFORMATION FOR SEQ ID NO: 74

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 15 (B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74

	TAACGGGCGT	CTCGATAGAA	AAACACGTGA	AAATCCCAAT	GATTATAAAC	50
20	AATCAATATA	CGATTTTGCT	GAAGCTGTAA	CAAAAGGTAT	TAAGGAACAA	100
	ACAAATAAAA	ATTAATAGGC	AACTTAACCA	GAATCGTTAA	AACTATATGA	150
	AGATTCTGGT	TTTTTAAATT	CAAAAAGTTT	TCTAAAAAAT	TTACTTGCTT	200
	TTTTAAGTAT	AGGTATAAAA	TACGATTGAT	TAAAACAGTA	AAGGAAATGA	250
	ATCATGAAAC	AATTAACTAA	GCCTTTTATAC	TTTTACCTAT	TACTTTTTAT	300
25	TACAACAACG	CTGATTGGCG	CGTTACTATT	ATATTTGCCA	ATCACAGGTA	350
	AACATCCTAT	TGATTTTGTG	GACGCCCGTT			380

30 2) INFORMATION FOR SEQ ID NO: 75

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75

45	GCAATCTTGG	TCGTATCAGC	GACAGATGGC	CCAATGCCAC	AAACACGGGA	50
	GCATATTTTG	CTTTCTCGTC	AAGTGGGTGT	GAAACATTG	ATCGTCTTTT	100
	TGAATAAGAC	GGACCTTGTC	GATGATGACG	AGTTGATCGA	TTTAGTTGAA	150
	ATGGAAGTCA	GAGAATTGCT	GACTGAATAT	GATTTTCCTG	GCGACGACAT	200
50	TCCTGTGATC	AAGGGCTCTG	CGTTAAAAGC	CTTGGAAGGG	GACCCAGATG	250
	CTGAAGCAGC	GATCTTAACG	CTGATGGATA	CGGTAGATGA	ATATATCCCA	300
	ACGCCAGAAC	GTGATACTGA	CAAACCATG	TTGTTACCGA	TCGAAGATGT	350
	CTTTTCGATC	ACAGGACGGG	GGACCGTTGC	TTCTGGTCGG	ATCGATCGCG	400
	GCATGGTAAA	AGTCGGGGAT	GAAGTAGAAA	TCGTCGGAAT	CAAACCTGAA	450
55	ACACAAAAAG	CAGTCGTGAC	AGGGGTAGAA	ATGTTCCGCA	AAACGATGGA	500
	CTTCGGAGAA	GCTGGCGATA	ACGTAGGGGT	ATTGTTACGG	GGCATCACCC	550
	GTGATGAAAT	TGAACGTGGC	CAAGTGTTAG	CAAAACCAGG	TTCTATCACA	600
	CCGCATACGA	AATTCCAAGC	GGAAGTCTAT	GTGTTGACAA	AAGAAGAAGG	650
60	CGGTCGCCAT	ACCCCA				666

2) INFORMATION FOR SEQ ID NO: 76

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: ATCC 49573

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76

20 TGGTGC GATT TTAGTTGTAT CCGCAACAGA TGGTCCAATG CCTCAAACCC 50
 GGGAACATAT CTTGCTTTTCG AGACAAGTTG GTGTGAAACA TCTGATTGTT 100
 TTCTTGAACA AAATCGATTT AGTCGATGAC GAAGAATTGA TTGATTTAGT 150
 AGAAATGGAA GTAAGAGAAC TGCTATCTGA ATATAATTTT CCAGGGGATG 200
 ACATTCTGT TATCAAAGGT TCGGCATTAA AAGCGTTGGA AGGAGACCCT 250
 GATGCAGAAG CTGCCATCAT GGAATTAATG GATACAGTAG ACAGCTATAT 300
 25 CCCAACACCT GAGCGTGATA CAGACAAACC ATTACTCTTG CCAGTTGAAG 350
 ATGTCTTTTC GATTACTGGA CGAGGAACAG TTGCTTCCGG ACGGATCGAT 400
 CGGGGAACAG TTCGGGTAGG CGATGAAGTA GAAATCGTCG GTATCAAACC 450
 TGAAACCCAA AAAGCTGTAG TGACAGGCGT CGAAATGTTC CGCAAGACGA 500
 TGGACTTTGG GGAAGCCGGT GACAATGTAG GTGTCTTGCT GAGAGGGATC 550
 30 ACTCGTGACG AAATTGAACG AGGACAAAGT TTGGCTAAAC CAGGTTTCGAT 600
 CACACCACAT ACAAATTC AAGCAGAAGT TTATGTATTG ACGAAAGAAG 650
 AAGGTGGTCG TCATACACCA TTCTTCAACA ACTATCGTCC ACAATTTTAT 700
 TTCCGTACAA CGGATGTGAC AGGGAACATT ACATTGCCTG AAGGAACAGA 750
 A 751

35

2) INFORMATION FOR SEQ ID NO: 77

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ehrlichia canis*
 (B) STRAIN: Florida

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77

55 TGCAGCAATA TTAGTAGTGT CTGCAACTGA TGGAGCAATG CCACAAACAA 50
 GAGAACATAT ATTATTAGCA AAGCAAGTAG GTGTAAAAGA TATAGTAGTG 100
 TGGATGAATA AGTGTGATGT TGTAGATGAT GAAGAAATGT TGTCATTAGT 150
 TGAAATGGAA ATAAGGGAAT TGTTATCAAA ATATGGGTAT CCTGGGGATG 200
 ATATAGATGT AGTTAGAGGA TCTGCAGTTA AAGCATTAGA AGAAGAAACA 250
 GGCTCAGGTG TGTGGAGTGA AAAAATAATG GAATTGATGA ATGCTTTAGA 300
 60 AAAAATAAGT TTACCAGTAA GAGAAAAAGA TAAGCCATTT TTAATGTCAA 350

	TAGAAGATGT	GTTTTCAATA	CCTGGAAGAG	GTACAGTAGT	AACAGGAAGA	400
	ATAGAAAGAG	GAGTAATTAG	AGTAGGGGAT	AAAATAGAGA	TAGTAGGATT	450
	GCGTGAGATA	CAAAGTACAG	TATGTACAGG	TGTTGAAATG	TTTCATAAAG	500
	CATTAGATGC	AGGAGAAGCA	GGGGATAATG	CTGGAATATT	GTTAAGAGGG	550
5	ATAAAAAAAG	AAGATGTAGA	AAGAGGGCAA	GTATTGAGTG	CACCTGGACA	600
	GATACATTCA	TATAAGAGAT	TTAAGGCAGA	GGTATATATA	TTGAAAAAAG	650
	AAGAAGGAGG	AAGACATACT	CCATTTTCT	CAAATTACCA	GCCGCAATTT	700
	TATGTTAGAA	CAACAGATGT	AACAGGGAAT	ATAAAGTTAC	CAGAAGGAGT	750
	AGAAATGGTA	ATGCCAGGGG	ATAATATAAA	TATCGAAGTG	AGTTTGGATA	800
10	AGCCTGTTGC	TATTGATCAA	GGATTGAGAT	TTGC		834

2) INFORMATION FOR SEQ ID NO: 78

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 23511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78

30	CGGCGCGATC	CTGGTAGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
35	GAGTGGGAAG	CGAAAATCCT	GGAAGTGGCT	GGCTTCCTGG	ATTCTTAYAT	300
	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GA CTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
40	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
45	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGT				817

50 2) INFORMATION FOR SEQ ID NO: 79

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia fergusonii*
 (B) STRAIN: ATCC 35469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79

```

5      CGATCCTGGT AGTTGCTGCG ACTGACGGCC CGATGCCGCA GACTCGTGAG      50
      CACATCCTGC TGGGTCGTCA GGTAGGCGTT CCGTACATCA TCGTGTTTCCT      100
      GAACAAGTGC GACATGGTTG ATGACGAAGA GCTGCTGGAA CTGGTTGAAA      150
      TGGAAGTTCG TGAAGTCTCT TCTCAGTACG ACTTCCCAGG CGACGACACT      200
10     CCGATCGTTC GTGGTTCTGC TCTGAAAGCG CTGGAAGGCG ACGCAGAGTG      250
      GGAAGCGAAA ATCCTGGAAC TGGCTGGCTT CCTGGATTCT TACATTCCGG      300
      AACCAGAGCG TGCATTGAC AAGCCGTTCC TGCTGCCGAT CGAAGACGTG      350
      TTCTCCATCT CCGGTCGTGG TACCGTTGTT ACCGGTCGTG TAGAACGCGG      400
      TATCATCAAA GTTGGTGAAG AAGTTGAAAT CGTTGGTATC AAAGAGACTC      450
15     AGAAGTCTAC CTGTACTGGC GTTGAAATGT TCCGCAAAC TCTGGACGAA      500
      GGCCGTGCTG GTGAGAACGT AGGTGTTCTG CTGCGTGGTA TCAAACGTGA      550
      AGAAATCGAA CGTGGTCAGG TACTGGCTAA GCCGGGCACC ATCAAGCCGC      600
      ACACCAAGTT CGAATCTGAA GTGTACATTC TGTCAAAGA TGAAGGCGGT      650
      CGTCATACTC CGTTCTTCAA AGGCTACCGT CCGCAGTTCT ACTTCCGTAC      700
20     TACTGACGTG ACTGGTACCA TCGAACTGCC GGAAGGCGTA GAGATGGTAA      750
      TGCCGGGCGA CAACATCAAA ATGGTTGTTA CCCTGATCCA CCCGATCGCG      800
      ATGGACGACG GTCTGCGTTT CGCAA      825
  
```

25 2) INFORMATION FOR SEQ ID NO: 80

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia hermannii*
 (B) STRAIN: ATCC 33650

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80

```

      GCGCGGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG      50
      TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT      100
      TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT      150
45     GAGATGGAAG TTCGCGAACT GCTGTCCCAG TACGATTTCC CGGGCGACGA      200
      CACCCCGATC GTTCGTGGTT CCGCGCTGAA AGCGCTGGAA GGCGAAGCAG      250
      AGTGGGAAGA GAAAATCATC GAACTGGCTG GCTACCTGGA TTCCTATATC      300
      CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CTATCGAAGA      350
      CGTATTCTCC ATCTCCGGCC GTGGTACCGT TGTTACCGGT CGTGTAAGAGC      400
50     GCGGTATCAT CAAAGTGGGT GAAGAAGTTG AAATCGTGGG TATCAAAGAT      450
      ACTGCGAAAT CAACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
      CGAAGGCCGT GCGGGCGAGA ACGTGGGTGT TCTGCTGCGT GGTATCAAAC      550
      GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG TTCCATCAAG      600
      CCKCACACCA AGTTCGAATC TGAAGTGTA ATTCTGTCCA AAGACGAAGG      650
55     CGGCCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC      700
      GTACAACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTTGAGATG      750
      GTAATGCCGG GCGACAACAT CAAATGGTT GTTACCCTGA TCCACCCGAT      800
      CGCGATGGAC GACGGTCTGC GTTTCGCAA      829
  
```

60

2) INFORMATION FOR SEQ ID NO: 81

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia vulneris*
 (B) STRAIN: ATCC 33821

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
20	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAGATGGAA	GTGCGTGAAC	TTCTGTCCCA	GTACGACTTC	CCGGGCGACG	200
	ACACCCCGAT	CATTCGTGGT	TCTGCGCTGA	AAGCGCTGGA	AGGCGAAGCT	250
	GAGTGGGAAG	AGAAAATCGT	TGAGCTGGCT	GGCTACCTGG	ATTCTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
25	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAARGTKGG	TGAAGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	TACTGCGAAA	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCG	TGCAGGCGAG	AACTGCGGCG	TTCTGCTGCG	TGGTATCAAG	550
	CGTGAAGAGA	TCCAGCGTGG	CCAGGTTCTG	GCTAAGCCGG	GCTCAATCAA	600
30	GCCGCACACC	AAGTTCGAAT	CCGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	CACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAACTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCATCCGA	800
35	TCGCGATGGA	CGACGG				816

2) INFORMATION FOR SEQ ID NO: 82

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eubacterium lentum*
 50 (B) STRAIN: ATCC 43055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82

	CGGCGCCTCC	TCGTTATCGC	CGCCACCGAC	GGCCCGATGG	CCCAGACCCG	50
55	CGAGCACATC	CTGCTCGCCC	GTCAGGTCGG	CGTGCCCTAC	ATCGTGGTCT	100
	TCCTGAACAA	GTGCGACATG	GTCGACGACG	AGGAGCTCCT	CGAGCTCGTC	150
	GAGATGGAAG	TTGCGGAGCT	GCTCGACTCT	TACGAGTTCC	CGGGCGACGA	200
	CACCCCGATC	ATCCGCGGCT	CCGCTTTGAA	GGCCCTCGAG	GGCGACAAAG	250
	AGTGGCAGGA	GAAGGTCTGG	GAGCTCATGG	ACGCCGTCGA	CTCCTACATC	300
60	CCGACGCCCG	AGCGCATGGT	CGACAAGCCG	TTCCTGATGG	CCGTCGAGGA	350

	CACGATGACC	ATCACCGGCC	GCGGCACCGT	TGCCACCGGT	CGTGTGGAGC	400
	GTGGTACGCT	GCATGTCAAC	GACCCGCTGG	AGATCGTCGG	TATCAAGGAG	450
	ACCCAGAAC	CGGTCTGCAC	CGGTATCGAG	ATGTTCCGCA	AGCTGCTCGA	500
	CGAGGCTCAG	GCCGGCGACA	ACATCGGCTG	CCTGCTCCGC	GGTGTCAAGC	550
5	GCGAGGAGAT	CGTTCGCGGC	CAGGTTCTCT	GCAAGCCCGG	TAGCGTGACC	600
	CCGCACACCG	AGTTCGAGGG	TCAGGTCTAC	ATCCTGACGA	AGGAAGAGGG	650
	CGGCCGCCAC	ACGCCGTTCT	TCGACGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GCACGACGGA	CGTGACGGGT	GTTGCCACCC	TTCCCGAGGG	CACCGAGATG	750
	GTCATGCCGG	GCGACAACGT	GGAGATCAAG	GGCGAGCTCA	TTCACCCGAT	800
10	CGCCAGGAAG	AGGGCTGCGT	TCGCTAAC			828

2) INFORMATION FOR SEQ ID NO: 83

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eubacterium nodatum*
 (B) STRAIN: ATCC 33099

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83

30	GGAGCAATTC	TGGTTTGTGC	AGCAACKGAC	GGACCAATGC	CTCAGACAAG	50
	AGAACATATC	CTTTTGTCAA	GGCAGGTAGG	AGTGCCATAT	ATCATCGTAT	100
	TCCTGAATAA	ATGTGACATG	GTGGATGAYG	AAGAGCTTCT	GGACTTGCTA	150
	GAGATGGAAG	TAAGAGAACT	TCTCAGTGAG	TATGAATTCC	CGGGAGATGA	200
	TACCCCGATA	GTAAGAGGTT	CAGCCCTGAA	GGCACTGGAA	GAACCCAATG	250
35	GAGAATGGGC	AGACAAGATT	GTAAGAGCTGA	TGGAGGAAGT	AGATAAATAC	300
	ATTCTCTGAA	CAAAGAGAGA	TAACGACAAA	CCGTTCTCTGA	TGCCTGTAGA	350
	GGACGTATTC	TCAATAACAG	GAAGAGGAAC	AGTAGCGACA	GGAAGRGTTG	400
	AAAGAGGAAT	CCTGAAGGTC	GGTGATGAAG	TAGAAATCGT	GGGAATGAGC	450
	GAAGAGAGAA	GAAAGGTAAGT	AGTAACGGGA	GTTGAAATGT	TCAGAAAGCT	500
40	TCTGGATGAA	GCAGAGACAG	GAGACAACAT	CGGAGCACTG	CTGAGAGGAG	550
	TTCAGAGAAC	RGAGATCCAG	AGAGGTCAGG	TATTGGCRGC	ACCTGGAACG	600
	ATCAACCCAC	ATACAAAGTT	CAAGGGTCAG	GTATATGTAC	TGAAGAAGGA	650
	AGAAGGAGGA	AGGCATACGC	CGTTCTTCAA	YGGATACAGW	CCACAGTTCT	700
	ACTTCAGAAC	AACAGACGTA	ACAGGAGATT	TGCAGCTGCC	GGAAGGARCA	750
45	GAGATGTGCA	TGCCGGGAGA	TAATGTGGTA	ATGAACRTCA	GCCTGATCAC	800
	TCCGATTGCT	ATAGAAGAGG	GWCTGAGATT	TGCCA		835

50 2) INFORMATION FOR SEQ ID NO: 84

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM: *Ewingella americana*
 (B) STRAIN: ATCC 33852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84

```

5      GCGATCCTGG TTGTTGCTGC AACTGATGGC CCTATGCCAC AGACTCGTGA      50
      GCACATCCTG TTGGGTCGYC AGGTTGGCGT TCCATTCATG ATCGTATTCA      100
      TGAACAAATG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA      150
      ATGGAAGTTC GYGAACTTCT GTCTGCTTAC GATTTCCCAG GCGACGACAT      200
10     CCCAGTTGTT AAAGGTTTCA CGCTGAAAGC ACTGGAAGGC GAAGCAGAGT      250
      GGGAAAGCTAA GATCATCGAG CTGGCTGGCC ACCTGGATAG CTACATCCCA      300
      GAACCAGAGC GTGCGATTGA CAAGCCATTC CTGCTGCCAA TCGAAGACGT      350
      ATTCTCCATC TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAGCGCG      400
      GTATCATCAA AGTTGGCGAA GAAGTTGAAA TCGTTGGTAT CAAGGACACT      450
15     GTTAAGTCTA CTTGTACTGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA      500
      AGGCCGTGCY GGTGAGAACG TTGGTGTTC TCTGCGTGGT ATCAAGCGTG      550
      AAGACATCGA ACGTGGTCAG GTTCTGGCTA AACCAGGTTC AATCAAACCA      600
      CACACCACWT TYGACTCAGA AGTTTATATC CTGAGCAAAG ATGAAGGCGG      650
      CCGTCATACT CCGTTCCTCA AAGGCTACCG TCCACAGTTC TACTTCCGTA      700
20     CAACTGACGT GACCGGTACC ATCGAACTGC CAGAAGGCGT AGAGATGGTA      750
      ATGCCAGGTG ACAACATCAA CATGRTAGTT ACCCTGATCC ACCCAATCGC      800
      GATGGATGAC GGTCTGCGTT TCGCAA      826
  
```

25

2) INFORMATION FOR SEQ ID NO: 85

(i) SEQUENCE CHARACTERISTICS:

```

30     (A) LENGTH: 828 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Francisella tularensis*
 (B) STRAIN: LVS

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85

```

      TGGTGCTATT CTAGTATGTT CTGCTGCGGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT TCTGCTTTCT CGTCAAGTTG GTGTACCAA AATCGTTGTT      100
      TTCTTAAACA AGTGTGACAT GGTGATGAT GAAGAGTTAT TAGAGCTAGT      150
45     TGAGATGGAA GTTCGTGAGC TTTTAGATCA GTATGAGTTC CCAGGTGATG      200
      ACACTCCAGT TATTATGGGT TCAGCTCTTA GAGCTATTGA AGGTGACGAA      250
      GCTTACGTTG AGAAAATTGT TGAGCTAGTT CAAGCTATGG ATGACTATAT      300
      TCCTGCTCCT GAGCGTGATA CTGAGAAGCC ATTTATTCTT CCGATCGAAG      350
      ATGTATTCTC AATTTTCAGT CGTGGTACTG TTGTAAGTGG TCGTATTGAG      400
50     CGCGGTGTAG TTAACGTTGG TGATGAAGTT GAAGTTGTTG GTATTCGTCC      450
      AACTCAAAAA ACTACAGTAA CTGGTGTGGA AATGTTCCGT AAGCTTTTAG      500
      ATAGAGGGGA AGCTGGTGAT AACGTTGGTA TCCTAGTTCG TGGACTTAAG      550
      AGAGATGATG TTGAGCGTGG ACAAGTATTA TGTAAGCCAG GTTCAATTAA      600
      GCCACATACT AAGTTTGAAG CTGAGGTTTA TGTATTATCT AAAGAAGAGG      650
55     GTGGTAGACA TACTCCATTC TTCAAGGGAT ATAGACCACA ATTCTACTTC      700
      CGTACTACAG ACATTACTGG AGCTGTTGAG CTTCCAGAGG GTGTAGAAAT      750
      GGTATGCCT GGTGATAACG TTAAGATGAC TATCACTCTA ATTAACCCAA      800
      TCGCTAGGAT GAAGGGTTAC GTTTTGCA      828
  
```

60

2) INFORMATION FOR SEQ ID NO: 86

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*
 (B) STRAIN: ATCC 10953

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86

	CGGTGCTATC	ATCGTAGKTG	CTGCTACTGA	TGGTCCGATG	CCTCARACTC	50
	GTGAGCAYAT	CYTGCTGGCT	CGTCAGGTAA	ACGTWCKKAG	ACTGGTTGTA	100
20	TTCATGAACA	AGTGYGACAT	GGTAGACGAC	GCTGAAATGY	TGGAACCTCGT	150
	TGAAATGGAA	ATGCGTGAAC	TGCTTTCAGC	YTACGAATTC	GAYGGYGACA	200
	ACACTCCKTT	CATTCAGGGT	TCTGCTCTTG	GTGCRTTGAA	YGGCGTTGAA	250
	AAGTGGGAAG	AGAAGGTTAT	GGANCTGATG	GATGCTTGCG	ACACTTGGAT	300
	TCCTTTGCCT	CCGCGTGATA	TTGAYAAACC	GTTCTTGATG	CCGTTTGAAG	350
25	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCTACTGG	TCGTATCGAA	400
	GCTGGTGTTA	TCCATGTAGG	TGACGAAGTT	GAAATCCTCG	GTTTGGGTGA	450
	AGACAAGAAG	TCTGTTGTAA	CTGGTGTTGA	AATGTTCCGC	AAGTTGCTGG	500
	ATCAAGGTGA	AGCTGGTGAC	AACGTAGGTY	TGTTGCTCCG	TGGTATCGAC	550
	AAGAACGAAA	TCAAACGTGG	TATGGTTCTT	TGTAAGCCCG	GTCAGATTAA	600
30	ACCTCACTCT	AAGTTCAAAG	CTTCTATCTA	CGTTTTGAAG	AAAGAAGAAG	650
	GTGGTCGTCA	CACTCCGTTT	CACAACAAAT	ACCGTCCTCA	GTTCTATCTG	700
	CGTACTATGG	ACTGTACAGG	TGAAATCWCT	CTTCCGGAAG	GAAGTGAAT	750
	GGTAATGCCT	GGTGATAACG	TAGAAATCAC	TGTAGAACTG	ATCTACCCGG	800
35	TAGCATTGAA	CGTAGGTTTG	CGTTTCGCT			829

2) INFORMATION FOR SEQ ID NO: 87

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gemella haemolysans*
 50 (B) STRAIN: ATCC 10379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87

	CTATCTTAGT	AATCGCTGCT	ACAGATGGAC	CAATGGCTCA	AACTCGTGAG	50
55	CACATCCTAT	TATCTCGTAA	CGTTGGAGTA	CCAAAAATCG	TTGTATTCTT	100
	AAACAAATGT	GATATGGTTG	ATGACGAAGA	GTTATTAGAA	TTAGTTGAAA	150
	TGGAAGTTTCG	TGAACTATTA	TCTGAATACG	GATTCGACGG	AGATGAACCTA	200
	CCAGTAATCA	AAGGTTCTGC	TCTTAAAGCT	CTTGAAGGAG	ATGCAGATGC	250
	AGAAAAAGCT	ATCATCGAAT	TAATGGAAAC	AGTTGACGAA	TACATCCCAA	300
60	CTCCAGAACG	TGATAACGCT	AAACCATTCA	TGATGCCAGT	TGAGGACGTA	350

	TTCTCAATCA	CAGGTCGTGG	TACAGTTGCT	ACTGGACGTG	TTGAACGTGG	400
	ACAAGTTAAA	GTTGGAGACG	TAGTAGAAAT	CGTTGGATTA	ACTGAAGAAC	450
	CAGCTTCAAC	TACTGTAAAC	GGTGTGAAA	TGTTCCGTAA	ATTATTAGAT	500
	TACGCTGAAG	CAGGAGATAA	CATCGGTGCA	TTATTACGTG	GTGTTGCTCG	550
5	TGAAGACATC	GAACGTGGAC	AAGTTTTAGC	AGCTCCTAAA	ACAATCACTC	600
	CACACACTCA	ATTCGTAGCT	GACGTGTACG	TATTATCTAA	AGAAGAAGGT	650
	GGACGTCACA	CTCCATTCTT	CACAACTAC	CGTCCTCAAT	TCTACTTCCG	700
	TACTACTGAC	GTAACCTGGT	TAGTTACTTT	ACCAGAAGGT	ACTGAAATGG	750
	TAATGCCTGG	GGATAACGTA	TCAATCAACG	TAGAACTTAT	TTCTCCAATC	800
10	GCGATCGAAG	AAGGAACTCG	TTTCTCAA			828

2) INFORMATION FOR SEQ ID NO: 88

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Gemella morbillorum*
 (B) STRAIN: ATCC 27824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88

30	TCTTAGTAAT	CGCTGCTACA	GATGGTCCTA	TGGCTCAAAC	TCGTGAACAC	50
	ATCCTATTAT	CTCGTAACGT	TGGAGTACCT	AAAATTGTTG	TATTCTTAAA	100
	CAAATGTGAT	ATGGTTGATG	ACGAAGAGTT	ATTAGAATTA	GTAGAAATGG	150
	AAGTTCGTGA	ACTATTATCT	GAATACGGAT	TTGATGGAGA	TGAAC TACCA	200
	GTAATCAAAG	GTTTCAGCTCT	TAAAGCTCTT	GAAGGAGATG	CAGATGCTGA	250
35	AAAAGCTATC	ATCGAATTAA	TGGAAACAGT	TGACGAGTAC	ATCCCAACTC	300
	CAGAACGTGA	TAACGCTAAA	CCATTTATGA	TGCCAGTTGA	GGACGTGTTC	350
	TCAATCACAG	GTCGTGGTAC	AGTTGCTACT	GGACGTGTTG	AACGTGGACA	400
	AGTTAAAGTT	GGTGACGTAG	TAGAAATCGT	TGGATTAACT	GAAGAACCAG	450
	CTTCAACTAC	TGTAACAGGT	GTTGAAATGT	TCCGTAAATT	ATTAGATTAC	500
40	GCTGAAGCAG	GAGATAACAT	CGGTGCATTA	TTACGTGGTG	TTGCTCGTGA	550
	AGATATCGAA	CGTGGACAAG	TTT TAGCAGC	TCCTAAAACA	ATCACTCCAC	600
	ATACTCAATT	CGTAGCTGAT	GTGTACGTAT	TATCTAAAGA	AGAAGGTGGA	650
	CGTCACACTC	CATTCTTCAC	AACTACCGT	CCACAATTCT	ACTTCCGTAC	700
	TACTGACGTA	ACTGGTGTAG	TTACTTTACC	AGAAGGTACT	GAAATGGTAA	750
45	TGCCTGGGGA	CAACGTATCA	ATCAACGTAG	AACTTATTTC	TCCAATCGCT	800
	ATCGAAGAAG	GAAC TCGTTT	CTC			823

50 2) INFORMATION FOR SEQ ID NO: 89

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus actinomycetemcomitans*
 (B) STRAIN: ATCC 33384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89

```

5      GCTATCTTAG TAGTAGCAGC AACCGACGGT CCTATGCCAC AAACCTCGTGA      50
      GCACATCTTA TTAGGTCGCC AAGTAGGTGT TCCTTACATC ATCGTATTCT      100
      TAAACAAATG CGACATGGTA GATGACGAAG AGTTATTAGA ATTAGTTGAA      150
      ATGGAAGTTC GTGAACTTCT TTCTCAATAT GACTTCCCGG GCGATGACAC      200
10     CCCAATCGTA CGCGGTTCTG CATTAAAAGC GCTTGAAGGC GATGCCGCAT      250
      GGGAAGAAAA AATCCTTGAA TTAGCAAACC ATTTAGATAC TTACATCCCG      300
      GAACCTGAGC GTGCTATCGA CCAACCGTTC CTTCTTCCAA TTGAAGATGT      350
      GTTCTCTATC TCCGGTCGTG GTACCGTAGT AACGGGTCGT GTTGAGCGCG      400
      GTATCATCCG TACCGGTGAT GAAGTTGAAA TCGTGGGTAT CAAACCGACT      450
15     GCAAAAACCA CCGTAACCGG TGTTGAAATG TTCCGTAAAT TACTTGACGA      500
      AGGTCGTGCG GGTGAAAACA TCGGTGCATT ATTGCGTGGT ACTAAACGTG      550
      AAGAAATCGA ACGTGGTCAG GTATTGGCGA AACCGGGGTC AATCACCCCG      600
      CACACTGACT TCGAATCTGA AGTGACGTA TTGTCCAAAG AAGAAGGTGG      650
      TCGTCATACT CCATTCTTCA AAGGTTACCG TCCACAATTC TATTTCGGTA      700
20     CAACTGACGT AACCGGTACT ATCGAGTTAC CTGAAGGCGT GGAAATGGTT      750
      ATGCCTGGCG ATAACATCAA AATGACCGTA TCCTTAATTC ACCCAATTGC      800
      GATGGACCAA GGTTTACGTT TCGCTATCG      829
  
```

25

2) INFORMATION FOR SEQ ID NO: 90

(i) SEQUENCE CHARACTERISTICS:

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30     (A) LENGTH: 833 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
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(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Haemophilus aphrophilus
      (B) STRAIN: ATCC 33389
  
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40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90

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      TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCTTA CATCATCGTA      100
      TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT      150
45     TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGATG      200
      ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTTGCA      250
      GAATGGGAAG AAAAAATCCT TGAATTAGCA AACCACTTAG ATACTTACAT      300
      TCCTGAGCCA CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATTGAAG      350
      ACGTGTTCTC TATCTCCGGT CGTGGTACTG TAGTAACAGG TCGTGTTGAG      400
50     CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC      450
      GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG      500
      ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGCACTAAA      550
      CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GCTCAATCAC      600
      TCCGCACACT GATTTCGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG      650
55     GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTT      700
      CGTACAACCTG ACGTAACCGG TACTATCGAG TTACCGGAAG GCGTGGAAT      750
      GGTATATGCT GGCATAACA TCAAAATGAC TGTATCCTTA ATCCACCCAA      800
      TCGCGATGGA CCAAGGTTTA CGTTTCGCTA TCG      833
  
```

60

2) INFORMATION FOR SEQ ID NO: 91

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 815 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus ducreyi*
 (B) STRAIN: DSM 8925

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91

	CGGCGCTATC	TTAGTTGTAG	CAGCAACTGA	TGGTCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTATTAGGC	CGCCAAGTTG	GTGTTCCCTTA	CATCATCGTA	100
20	TTCTTAAATA	AATGCGATAT	GGTAGATGAT	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTTTCTCA	ATATGATTTC	CCAGGTGACG	200
	ATACTCCTAT	CGTTCGTGGT	TCAGCATTAC	AAGCATTAAG	TGGTGTGCCT	250
	GAGTGGGAAG	AAAAAATCAT	TGAATTAGCA	CAACACTTAG	ATTCTTATAT	300
	CCCTGAGCCT	GAGCGTGCGA	TTGATAAACC	TTTCTTATTA	CCAATCGAAG	350
25	ACGTATTCTC	AATTTCAGGT	CGTGGTACAG	TAGTAACCGG	TCGTGTTGAG	400
	CGTGGTATCA	TCAAATCAGG	TGAAGAAGTT	GAAATCGTAG	GGATTAAAGA	450
	AACGACAAAA	ACAACAGTAA	CCGGTGTGTA	GATGTTCCGT	AAACTATTAG	500
	ACGAAGGTCG	TGCGGGTGAA	AACGTAGGTG	CCTTATTACG	TGGTACTAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAAGTATTA	GCGAAACCAG	GTACAATTAC	600
30	ACCACACACT	GATTTTGAAT	CAGAAAGTTA	TGTATTATCA	AAAGAAGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGGTT	ATCGTCCTCA	GTTCTACTTC	700
	CGYACAACGG	ACGTAACAGG	AACGATTGAA	TTACCTGAAG	ATGTTGAGAT	750
	GGTAATGCCT	GGTGATAATA	TCAAGATGAC	AGTAAGCTTA	ATTCACCCTA	800
35	TCGCGATGGA	CGAAG				815

2) INFORMATION FOR SEQ ID NO: 92

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus haemolyticus*
 50 (B) STRAIN: ATCC 33390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92

	TGGTGCTATC	TTAGTAGTAG	CAGCAACTGA	TGGTCCAATG	CCACAAACCTC	50
55	GTGAGCACAT	CTTATTAGGT	CGCCAAGTAG	GTGTTCCATA	CATCATCGTA	100
	TTCTTAAACA	AATGCGACAT	GGTAGATGAC	GAAGAGTTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTTCGTGAAC	TTCTTTCTCA	ATATGACTTC	CCAGGTGACG	200
	ATACACCAAT	CGTACGTGGT	TCTGCATTAC	AAGCATTAAG	TGGCGTAGCA	250
	GAATGGGAAG	AAAAAATCCT	TGAGTTAGCA	AACCACTTAG	ATACTTACAT	300
60	CCCAGAACCA	GAGCGTGCAA	TTGACCAACC	GTTCTTCTT	CCAATCGAAG	350

	ATGTGTTCTC	AATCTCAGGT	CGTGGTACAG	TAGTAACTGG	TCGTGTAGAA	400
	CGTGGTATCA	TCCGTACTGG	TGATGAAGTA	GAAATCGTAG	GTATCAAAGA	450
	TACAGCAAAA	ACTACTGTAA	CGGGTGTGTA	AATGTTCCGT	AAATTACTTG	500
	ACGAAGGTCG	TGCAGGTGAA	AACATCGGTG	CATTATTACG	TGGTACCAAA	550
5	CGTGAAGAAA	TCAACGTGG	TCAAGTATTA	GCGAAACCAG	GTTCAATCAC	600
	GCCACACACT	GACTTCGAAT	CAGAAGTTTA	TGTATTATCA	AAAGAAGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGGTT	ACCGTCCACA	ATTCTATTTC	700
	CGTACAACCTG	ACGTAACCTGG	TACTATCGAG	TTACCAGAAG	GCGTAGAAAT	750
	GGTAATGCCA	GGCGATAACA	TCAAGATGAC	AGTAAGCTTA	ATCCACCCAA	800
10	TCGCGATGGA	CCAAGGTTTA	CGTTTCGCAA			830

2) INFORMATION FOR SEQ ID NO: 93

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Haemophilus parahaemolyticus*
 (B) STRAIN: ATCC 10014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93

30	TCTTAGTAGT	AGCAGCAACA	GACGGTCCAA	TGCCACAAAC	TCGTGAGCAC	50
	ATCTTATTAG	GTCGCCAAGT	AGGTGTTCCA	TACATCATCG	TATTCTTAAA	100
	CAAATGCGAT	ATGGTTGACG	ATGAAGAATT	ATTAGAATTA	GTTGAAATGG	150
	AAGTGCCTGA	ACTTCTTTCA	CAATATGACT	TCCCAGGTGA	TGACACGCCA	200
	GTAGTACGTG	GTTCAGCGTT	ACAAGCGTTA	AACGGCGTAG	CAGAGTGCGA	250
35	AGAAAAAATT	CTTGAATTAG	CAAACCACTT	AGATACATAC	ATCCCAGAGC	300
	CAGAGCGTGC	GATTGATAAA	CCATTCTTAT	TACCAATCGA	AGACGTATTC	350
	TCAATCTCAG	GTCGTGGTAC	AGTAGTAACA	GGTCGTGTTG	AGCGTGGTAT	400
	CATCAAAGCG	GGTGAAGAAG	TTGAAATCGT	AGGTATCAAA	GACACTGCCA	450
	AAACAACAGT	AACTGGCGTG	GAAATGTTCC	GTAAATTATT	AGACGAAGGT	500
40	CGTGCGGGTG	AAAACGTTGG	TGCATTATTA	CGTGGTACAA	AACGTGAAGA	550
	AATCGAACGT	GGTCAAGTGT	TAGCGAAACC	AGGTACAATT	ACACCACACA	600
	CAGACTTCGA	ATCAGAAGTG	TACGTATTAT	CAAAAGAAGA	AGGTGGTTCGT	650
	CACACTCCAT	TCTTCAAAGG	TTACCGTCCA	CAATTCTACT	TCCGTACAAC	700
	TGACGTAAGT	GGTACTATTG	AATTACCAGA	AGGCGTAGAA	ATGGTAATGC	750
45	CAGGCGATAA	CATCAAAATG	ACAGTATCAT	TAATCCACCC	AATCGCGATG	800
	GACGAAGGTT	TACGTTTTGC	GATT			824

50 2) INFORMATION FOR SEQ ID NO: 94

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus parainfluenzae*
 (B) STRAIN: ATCC 7901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94

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5      TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTTCCTTA CATCATCGTG      100
      TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT      150
      TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGACG      200
10     ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTWGCA      250
      GAATGGGAAG AAAAAATCCT TGAATTAGCT AGCCACTTAG ATTCTTACAT      300
      TCCTGAGCCT CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATCGAAG      350
      ACGTGTTCTC TATCTCCGGT CGTGGTACAG TAGTAACAGG TCGTGTTGAG      400
      CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC      450
15     GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG      500
      ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACYAAA      550
      CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GTTCAATCAC      600
      TCCACACACT GATTTCGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG      650
      GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTTC      700
20     CGTACAAC TG ACGTAACCGG AACTATCGAA TTACCGGAAG GCGTGGAAT      750
      GGTTATGCCT GGTGATAACA TCAAAATGAC TGTATCCTTA ATCCACCCAA      800
      TCGCGATGGA CCAAGGTTTA CGTTTCGCTA TCG      833
  
```

25 2) INFORMATION FOR SEQ ID NO: 95

(i) SEQUENCE CHARACTERISTICS:

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30     (A) LENGTH: 824 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
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(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

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      (A) ORGANISM: Haemophilus paraphrophilus
      (B) STRAIN: ATCC 29241
  
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40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95

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      TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTTCCTTA CATCATCGTA      100
      TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT      150
45     TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGACG      200
      ATACGCCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTTGCA      250
      GAATGGGAAG AAAAAATCCT TGAATTAGCA AACCATTGG ATACTTACAT      300
      TCCTGAGCCA CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATCGAAG      350
      ACGTGTTCTC TATCTCCGGT CGTGGTACAG TAGTAACAGG TCGTGTTGAG      400
50     CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC      450
      GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG      500
      ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACCAA      550
      CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GTTCAATCAC      600
      TCCACACACT GATTTCGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG      650
55     GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTTC      700
      CGTACAAC TG ACGTAACCGG TACTATCGAG TTACCGGAAG GTGTGGAAT      750
      GGTAATGCCT GGCATAACA TCAAAATGAC CGTATCCTTA ATCCACCCAA      800
      TCGCGATGGA CCAAGGTTTA CGTT      824
  
```

60

2) INFORMATION FOR SEQ ID NO: 96

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus segnis*
 (B) STRAIN: ATCC 33393

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96

	GCTATCTTAG	TAGTAGCAGC	AACTGATGGT	CCTATGCCAC	AAACTCGTGA	50
	GCACATCTTA	TTAGGTCGCC	AAGTAGGTGT	TCCTTACATC	ATCGTATTCT	100
20	TAAACAAATG	CGACATGGTA	GATGACGAAG	AGTTATTAGA	ATTAGTTGAA	150
	ATGGAAGTTC	GTGAACTTCT	TTCTCAATAT	GACTTCCCAG	GTGATGATAC	200
	TCCAATCATT	CGTGGTTCTG	CATTACAAGC	GTTAAACGGC	GTAGCAGAAT	250
	GGGAAGAAAA	AATCCTTGAA	TTAGCTCAAG	CATTAGATAC	TTACATTCCCT	300
	GAACCTGAGC	GTGCAATCGA	CCAACCGTTC	CTTCTTCCAA	TTGAAGACGT	350
25	GTTCTCAATC	TCTGGTTCGTG	GTACTGTAGT	AACAGGTCGT	GTAGAGCGTG	400
	GTATCATCCG	TACCGGTGAT	GAAGTTGAAA	TCGTTGGTAT	CAAACCAACT	450
	GCGAAAACAA	CCGTAACCGG	TGTTGAAATG	TTCCGTAAAT	TACTTGACGA	500
	AGGTCGTGCA	GGTGAAAACA	TCGGTGCATT	ATTACGTGGT	ACTAAACGTG	550
	AAGAAATCGA	ACGTGGTCAA	GTATTAGCGA	AACCGGGTTC	AATCACTCCA	600
30	CACACTGACT	TCGAATCTGA	AGTGTACGTA	TTATCTAAAG	AAGAAGGTGG	650
	TCGTCTAACT	CCATTCTTCA	AAGGTTACCG	TCCACAATTC	TATTTCCGTA	700
	CAACTGACGT	AACCGGTACT	ATCGAGTTAC	CGGAAGGCGT	GGAAATGGTT	750
	ATGCCTGGCG	ATAACATCAA	AATGACCGTA	TCCTTAATCC	ACCCAATCGC	800
35	GATGGACCAA	GGTTTACG				818

2) INFORMATION FOR SEQ ID NO: 97

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 763 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Hafnia alvei*
 50 (B) STRAIN: ATCC 13337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97

	CGGCGCTATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCTATG	CCTCAGACTC	50
55	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTTG	GCGTTCCTTW	CATCATCGTR	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTCTGTGAAC	TTCTGTCTCA	GTACGACTTC	CCWGGYGATG	200
	ATACTCCAAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGYGMACCT	250
	GAGTGGGAAG	CTAAGATCGT	AGAACTGGCT	GAAACTCTGG	ATTCTTACAT	300
60	YCCACARCCA	GAACGTGCTA	TCGAYAAGCC	ATTCTTGCTG	CCAATCGAAG	350

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ACGTATTCTC TATCTCTGGC CGTGGTACWG TTGTTACCGG TCGTGTAGAG      400
CGCGGTATCG TTAAAGTTGG TGAAGAAGTT GARATCGTTG GTATCAAAGA      450
TACCGTTAAA TCAACTTGTA CCGGCGTTGA AATGTTCCGT AAAC TGCTGG      500
ACGAAGGTCG TGCAGGCGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAG      550
5  CGTGAAGACA TCGAACGTGG TCAGGTTCTG GCTAAACCAG GYTCYATCAA      600
GCCACACACC AAGTTCGAAT CAGAAGTTTA TATTCTGAGC AAAGATGAAG      650
GCGGYCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC      700
CGTACAAC TG ACGTGACCGG TACCATCGAA TTGCCAGAAG GCGTGGAAT      750
GGTAATGCCA GGC                                          763
10

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2) INFORMATION FOR SEQ ID NO: 98

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15  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 828 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
20

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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25  (A) ORGANISM: Kingella kingae
      (B) STRAIN: ATCC 23330

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98

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30  CGGCGCAATC TTGGTATGTT CAGCAGCTGA CGGTCCTATG CCACAAACTC      50
      GCGAACACAT CTTGTTGGCT CGCCAAGTAG GTGTACCTTA TATCATCGTA      100
      TTCATGAACA AATGCGACAT GGTCGATGAT GCTGAGTTGT TGGAATTGGT      150
      TGAAATGGAA ATCCGTGACT TGTGTCTAG CTACGATTTT CCAGGCGACG      200
      ATTGCCCAAT CGTCAAGGT TCTGCATTGC GYGCAATTGGA AGGCGACGCT      250
      GCATACAAAG AAAAAATCTT TGAATTGGCT GCTGCTTTGG ATAGCTACAT      300
35  TCCTACTCCA GAACGTGCTG TTGATAAACC ATTCTTGTTG CCAATCGAAG      350
      ATGTATTCTC TATCTCTGGT CGTGGTACAG TAGTTACTGG TCGTGTAGAG      400
      CGCGGTATCA TCAAAGTAGG CGAAGAGATT GAAATCGTTG GTTTGAAAGA      450
      CACGCAAAAA ACCACTTGTA CTGGCGTGGA AATGTTCCGC AAATTGTTGG      500
      ACGAAGGTCA AGCTGGTGAT AACGTTGGTG TATTATTGCG TGGTACGAAG      550
40  CGTGAAGACG TTGAACGTGG TCAGGTATTG GCTAAACCAG GTTCTATCAC      600
      TCCGCACACT AAATTGGAAG CTGAAGTGTA TGTGTTGAGC AAAGAAGAAG      650
      GTGGCCGTCA TACGCCATTC TTCGCTAACT ACCGCCACA ATTCTACTTC      700
      CGTACGACTG ACGTAACTGG TGCAGTTACT TTGTCTGAGG GTGTGGAAAT      750
      GGTTATGCCA GCGGAAAACG TGAAAATCAC TGTTGAGTTG ATTGCACCTA      800
45  TCGCTAGGAA AACGTTTGC GTTTTGCG                                          828

```

2) INFORMATION FOR SEQ ID NO: 99

```

50  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 828 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
55  (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

60  (A) ORGANISM: Klebsiella ornithinolytica

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(B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99

5	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAGCTGGTT	150
	GAAATGGAAG	TCCGTGAGCT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACGCCGATC	GTTCTGTGGT	CCGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
10	ACTGGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTACCTGGA	TTCTTACATC	300
	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAAGAGC	400
	GCGGTATCAT	CAAAGTGGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
15	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCTATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACAACCTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
20	GTCATGCCCG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TTCACCCGAT	800
	CGCGATGGAC	GATGGTCTGC	GTTTCGCA			828

25 2) INFORMATION FOR SEQ ID NO: 100

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 749 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Klebsiella oxytoca</i>
(B)	STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100

40	GATGCCGCAG	ACTCGTGAGC	ACATCCTGCT	GGGTCGTCAG	GTAGGCGTTC	50
	CGTACATCAT	CGTGTTTCTG	AACAAGTGCG	ACATGGTTGA	TGACGAAGAG	100
	CTGCTGGAAC	TGGTTGAAAT	GGAAGTTTCG	GAAGTTCTGT	CTCAGTACGA	150
	TTTCCCGGGC	GACGACACTC	CGATCGTTTC	TGGTTCTGCT	CTGAAAGCGC	200
45	TGGAAGGCGA	CGCWGAGTGG	GAACKKAAAA	TCATCGAACT	GGCTGGCTTC	250
	CTGGATTCTT	ACATTCCGGA	ACCAGAGCGT	GCGATTGACA	AGCCGTTTCT	300
	GCTGCCGATC	GAAGACGTAT	TCTCCATCTC	CGGTCGTGGT	ACCGTTGTTA	350
	CCGGTCGTGT	AGAGCGCGGT	ATCATCAAAG	TTGGCGAAGA	AGTTGAAATY	400
	GTTGGTATYA	AAGACACTGC	TAAGTCTACC	TGTAAGTGGC	TTGAAATGTT	450
50	CCGCAAACTG	CTGGACGAAG	GCCGYGCTGG	TGAGAACGTT	GGTGTTCTGC	500
	TGCGTGGTAT	CAAACGTGAA	GAAATCGAAC	GTGGTCAGGT	ACTGGCTAAG	550
	CCGGGCTCTA	TCAAGCCGCA	CACCAAGTTC	GAATCTGAAG	TTTATATCCT	600
	GTCCAAAGAC	GAAGGCGGCC	GTCACACTCC	GTTCTTCAAA	GGCTACCGTC	650
	CGCAGTTCTA	CTTCCGTACA	ACTGACGTGA	CTGGCACCAT	CGAACTGCCG	700
55	GAAGGCGTAG	AGATGGTTAT	GCCGGGCGAC	AACATCAAAA	TGGTTGTTA	749

2) INFORMATION FOR SEQ ID NO: 101

60

61

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella planticola*
 (B) STRAIN: ATCC 33531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101

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15  TGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCCGATG CCGCAGACTC      50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTTCATGAC GAAGAGCTGC TGGAAGTGGT      150
    TGAAATGGAA GTTCGTGAGC TGCTGTCTCA GTACGACTTC CCGGGCGACG      200
    ACACTCCGAT CGTTCGTGGT TCCGCTCTGA AAGCGCTGGA AGGCGAAGCA      250
20  GACTGGGAAG CGAAAATCAT CGAACTGGCT GGCTACCTGG ATTCTTACAT      300
    CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCTATCGAAG      350
    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG      400
    CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
    TACTGCTAAR TCWACCTGTA CYGGCGTTGA AATGTTCCGC AAAGTCTGG      500
25  ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA      550
    CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCTCTATCAA      600
    GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGACGAAG      650
    GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
    CGTACAACCTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT      750
30  GGTAATGCCG GCGGACAACA TCAAAATGGT TGTTACCCTG ATTCACCCRA      800
    TCGCGATGGA CGACGGTCTG CGTTTCGCAA      830
  
```

35 2) INFORMATION FOR SEQ ID NO: 102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 (B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102

```

50  CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACT CGTGAGCACA      50
    TCCTGCTGGG TCGTCAGGTA GCGTTCCGT ACATCATCGT GTTCCTGAAC      100
    AAATGCGACA TGTTTGATGA CGAAGAGCTG CTGGAAGTGG TTGAGATGGA      150
    AGTTCGTGAA CTGCTGTCTC AGTACGATTT CCCGGGCGAC GACACCCCGA      200
55  TCGTTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAGTGGGAA      250
    GCGAAAATCA TCGAACTGGC TGGCCACCTG GATACCTATA TCCCGGAACC      300
    AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT      350
    CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC      400
    ATCAAAGTAG GTGAAGAAGT TGAAATCGTT GGTATCAAAG AAACCGCGAA      450
60  AACCACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC      500
  
```

```

      GTGCTGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA      550
      ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA ACCCGCACAC      600
      CAAGTTCGAA TCTGAAGTGT ACATCCTGTC CAAAGACGAA GGCGGCCGTC      650
      ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT      700
5     GACGTGACTG GCACCATCGA ACTGCCGGAA GGCGTAGAGA TGGTAATGCC      750
      GGGCGACAAC ATCAAAATGG TTGTTACCTT GATCCACCCG ATCGCGATGG      800
      ACGACG                                     806

```

10

2) INFORMATION FOR SEQ ID NO: 103

(i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 743 bases
15     (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Klebsiella pneumoniae subsp. pneumoniae
      (B) STRAIN: ATCC 13883

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25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103

```

      GCAGACTCGT GAGCACATCC TGCTGGGTCG TCAGGTAGGC GTTCCGTACA      50
      TCATCGTGTT CCTGAACAAA TGCGACATGG TTGATGACGA AGAGCTGCTG      100
      GAACTGGTTG AGATGGAAGT TCGTGAAGTG CTGTCTCAGT ACGATTTCCTC      150
30     GGGCGACGAC ACTCCGATCG TTCGTGGTTC TGCTCTGAAA GCGCTGGAAG      200
      GCGACGCAGA GTGGGAAGCG AAAATCATCG AACTGGCTGG CCACCTGGAT      250
      ACCTATATCC CGGAACCAGA GCGTGCGATT GACAAGCCGT TCCTGCTGCC      300
      GATCGAAGAC GTATTCTCCA TCTCCGGTCG TGGTACCGTT GTTACCGGTC      350
      GTGTAGAGCG CGGTATCATC AAAGTAGGTG AAGAAGTTGA AATCGTTGGT      400
35     ATCAAAGAAA CCGCGAAAAC CACCTGTACT GGC GTTGAAA TGTTCCGCAA      450
      ACTGCTGGAC GAAGGCCGTG CTGGTGAGAA CGTAGGTGTT CTGCTGCGTG      500
      GTATCAAACG TGAAGAAATC GAACGTGGTC AGGTACTGGC TAAGCCGGGC      550
      ACCATCAACC CGCACACCAA GTTCGAATCT GAAGTGTACA TCCTGTCCAA      600
      AGACGAAGGC GGCCGTCACA CTCCGTTCTT CAAAGGCTAC CGTCCGCAGT      650
40     TCTACTTCCG TACTACTGAC GTGACTGGCA CCATCGAACT GCCGGAAGGC      700
      GTAGAGATGG TAATGCCGGG CGACAACATC AAAATGGTTG TTA          743

```

45 2) INFORMATION FOR SEQ ID NO: 104

(i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 819 bases
50     (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

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      (A) ORGANISM: Klebsiella pneumoniae subsp.
                   rhinoscleromatis
      (B) STRAIN: ATCC 13884

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60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104

TGGTTGTTGC TGC GACTGAC GGCCCGATGC CGCAGACTCG TGAGCACATC 50
 CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA 100
 ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT GAGATGGAAG 150
 5 TTCGTGAACT RCTGTCTCAG TACGATTTC CGGGCGACGA CACCCCGATC 200
 GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGAAGC 250
 GAAAATCATC GAACTGGCTG GCCACCTGGA TACCTATATC CCGGAACCAG 300
 AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA CGTATTCTCC 350
 ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC GCGGTATCAT 400
 10 CAAAGTAGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAA ACCGCGAAAA 450
 CCACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT 500
 GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT 550
 CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAC CCGCACACCA 600
 AGTTCGAATC TGAAGTGATC ATCCTGTCCA AAGACGAAGG CGGCCGTAC 650
 15 ACTCCGTTCT TCAAAGGCTA CCGTCCGAG TTCTACTTCC GTACTACTGA 700
 CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG GTAATGCCGG 750
 GCGACAACAT CAAAATGGTT GTTACCCTGA TCCATCCGAT CGCGATGGAC 800
 GACGGTCTGC GTTTCGCAA 819

20

2) INFORMATION FOR SEQ ID NO: 105

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Kluyvera ascorbata*
 (B) STRAIN: ATCC 33433

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105

CGGCGCGATC CTGGTTGTTG CTGCGACTGA TGGCCCTATG CCACAGACTC 50
 GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTA CATCATCGTG 100
 40 TTCCTGAACA AATGYGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT 150
 TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGCGACG 200
 ATACTCCAAT CATCCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGATGCA 250
 GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT 300
 CCCAGAACCA GAACGTGCTA TCGATAAGCC GTTCCTGCTG CCAATCGAAG 350
 45 ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG 400
 CGCGGTATCA TCAAAGTTGG YGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
 CACCGCTAAG TCTACCTGTA CCGGCGTTGA AATGTTCCGC AAAGTCTGCTG 500
 ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA 550
 CGTGAAGAAA TCGAACGTGG TCAGGTTCTG GCTAAGCCAG GCTCTATCAA 600
 50 GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGACGAAG 650
 GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCACA GTTCTACTTC 700
 CGTACTACTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTTGAGAT 750
 GGTAATGCCA GCGACAACA TCAAGATGGT TGTGACTCTG ATCCACCCAA 800
 TCGCGATGGA CGACGGCCTG CGTTTCGCAA CC 832

55

2) INFORMATION FOR SEQ ID NO: 106

60 (i) SEQUENCE CHARACTERISTICS:

64

(A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera cryocrescens*
 (B) STRAIN: ATCC 33435

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106

	TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACTC	50
15	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
	TTCTTGAACA	AATGTGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTT	CCAGGCGACG	200
	ACACTCCTAT	CGTTCGTGGT	TCCGCGCTGA	AAGCGCTGGA	AGGCGACGCT	250
	GAGTGGGAAG	CAAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
20	CCCAGAACCA	GAGCGTGCGA	TTGATAAGCC	GTTCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	CACTGCTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
25	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCTAAGCCAG	GCTCCATCAA	600
	GCCGCACACC	AAATTCGAAT	CTGAAGTTTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCAA	800
30	TCGCGATGGA	CGACGGTCTG	CGTTTCGCAA			830

2) INFORMATION FOR SEQ ID NO: 107

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera georgiana*
 (B) STRAIN: ATCC 51603

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107

50	CGCGATCCTG	GTTGTTGCTG	CGACTGACGG	CCCGATGCCG	CAGACTCGTG	50
	AGCACATCCT	GCTGGGTCGT	CAGGTTGGCG	TTCCGTACAT	CATCGTGTTT	100
	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTTGA	150
	AATGGAAGTT	CGTGAAGTTC	TGTCTCAGTA	CGACTTCCCG	GGCGACGACA	200
	CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGACGCTGAG	250
55	TGGGAAGCGA	AAATCATCGA	ACTGGCGGGC	TTCTTGGATT	CTTACATCCC	300
	GGAACCAGAG	CGTGCGATTG	ACAAGCCGTT	CCTGCTGCCG	ATCGAAGACG	350
	TATTCTCCAT	CTCCGGTCGT	GGTACCGTTG	TTACCGGTCT	TGTAGAACGC	400
	GGTATCATCA	AAGTTGGCGA	AGAAGTTGAA	ATCGTTGGTA	TCAAAGACAC	450
	CGCTAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAA	CTGCTGGACG	500
60	AAGGCCGTGC	TGGTGAGAAC	GTTGGTGTTT	TGCTGCGTGG	TATCAAACGT	550

65

5	GAAGAAATCG	AACGTGGTCA	GGTACTGGCT	AAGCCGGGTT	CTATCAAGCC	600
	GCACACCAAG	TTCGAATCTG	AAGTGTACAT	TCTGTCCAAA	GACGAAGGCG	650
	GCCGTCATAC	TCCGTTCTTC	AAAGGCTACC	GTCCGCAGTT	CTACTTCCGT	700
	ACTACTGACG	TGACTGGCAC	CATCGAACTG	CCGGAAGGCG	TTGAGATGGT	750
	AATGCCGGGC	GACAACATCA	AAATGGTTGT	TACCCTGATC	CACCCGATCG	800
	CGAAGGACGA	AGGTCTGCGT	TTCGCA			826

10 2) INFORMATION FOR SEQ ID NO: 108

(i) SEQUENCE CHARACTERISTICS:

```

15      (A)   LENGTH: 803 bases
      (B)   TYPE: Nucleic acid
      (C)   STRANDEDNESS: Double
      (D)   TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactobacillus casei* subsp. *casei*
(B) STRAIN: ATCC 393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108

25	GCTGCTGATG	GCCCAATGCC	ACAAACTCGT	GAACATATCT	TACTTTCACG	50
	TCAAGTTGGT	GTTCCATACA	TCGTTGTATT	CATGAACAAA	TGTGACATGG	100
	TTGACGATGA	AGAATTACTA	GAATTAGTTG	AAATGGAAAT	TCGTGATCTA	150
	TTAACTGAAT	ATGAATTCCC	TGGCGATGAC	ATTCTGTAA	TCAAAGGTTT	200
30	AGCTCTTAA	GCACTTCAAG	GTGAAGCTGA	CTGGGAAGCT	AAAATTGACG	250
	AGTTAATGGA	AGCTGTAGAT	TCTTACATTG	CAACTCCAGA	ACGTGATACT	300
	GACAAACCAT	TCATGATGCC	AGTTGAGGAT	GTATTCTCAA	TCACTGGTCTG	350
	TGGAACAGTT	GCAACTGGAC	GTGTTGAACG	TGGACAAGTT	AAAGTTGGTG	400
	ACGAAGTAGA	AGTTATCGGT	ATTGAAGAAG	AGAGCAAAAA	AGTAGTAGTA	450
35	ACTGGAGTAG	AAATGTTCCG	TAAATYACTA	GATTACGCTG	AAGCTGGCGA	500
	CAACATTGGC	GCACTTCTAC	GTGGTGTTC	TCGTGAAGAT	ATCCAACGTG	550
	GTCAAGTATT	AGCTAAACCA	GGTTCGATTA	CTCCACACAC	TAACTTCAAA	600
	GCTGAAACTT	ATGTTTTTAAC	TAAAGAAGAA	GGTGAGCTGC	ACACTCCATT	650
	CTTCAACAAC	TACCGCCAC	AATTCTATTT	CCGTACTACT	GACGTAAC TG	700
40	GTATTGTTAC	ACTTCCAGAA	GGTACTGAAA	TGGTAATGCC	TGGTGATAAC	750
	ATTGAGCTTG	CAGTTGANCT	AATTGCACCA	ATCGCTATCG	AAGACGGTAC	800
	TAA					803

45 2) INFORMATION FOR SEQ ID NO: 109

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis* subsp. *lactis*
(A) STRAIN: ATCC 19435

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109

	CGGTGCAATC	CTCGTTGTTG	CTGCAACTGA	TGGACCAATG	CCACAAACTC	50
	GTGAACACAT	CTTGCTTTCA	CGTCAAGTTG	GTGTAAATA	CCTTATCGTC	100
	TTCCTTAACA	AGGCTGACCT	TGTTGATGAT	GAAGAATTGA	TGGAATCGT	150
5	TGAAATGGAA	GTTCGTGACC	TCTTGAGCGA	ATACGACTTC	CCAGGTGACG	200
	ATATTCTGT	AATCGCTGGT	TCAGCACTTG	GTGCTTTGAA	CGGTGAACCA	250
	CAATGGGTTG	CTAAAGTTGA	AGAATTGATG	GACATCGTTG	ATGAATACAT	300
	CCCAACTCCA	GAACGCGACA	CTGACAAACC	ACTCCTTCTT	CCAGTCGAAG	350
	ACGTATTCTC	TATCACTGGT	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAA	400
10	CGTGGTACTG	TTAAAGTTGG	TGACGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	AGAAACTAAA	AAAGCTGTTG	TTACTGGTAT	CGAAATGTTC	CGTAAAACAC	500
	TTACTGAAGG	TCTTGCTGGT	GATAACGTCG	GTGCACTTCT	CCGTGGTATC	550
	CAACGTGACG	AAATCGAACG	TGGTCAAGTT	ATTGCTAAAC	CAGGTTCAAT	600
	CACTCCACAC	AAACTTTTCG	AAGGTGAAGT	TTACGTATTG	AGCAAAGAAG	650
15	AAGGCGGACG	TCACACTCCA	TTCTTCGACA	ACTACCGTCC	TCAATTCTAC	700
	TTCCACACAA	CTGACGTTAC	TGGTTCAGTT	AAACTTCCAG	AAGGAACTGA	750
	AATGGTAATG	CCTGGTGACA	ACGTGCATAT	CGACGTTGAA	TTGATCCACC	800
	CAGTTGCGAT	CGAACAAGGT	ACTAC			825

20

2) INFORMATION FOR SEQ ID NO: 110

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 824 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leclercia adecarboxylata*

(B) STRAIN: ATCC 23216

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCAATGC	CTCAGACCCC	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCTTTC	ATCATCGTGT	100
40	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGT	150
	GAGATGGAAG	TTCGTGAACT	YCTGTCCCAG	TACGACTTCC	CGGGCGACGA	200
	CACCCCAATC	GTTCGTGGTT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
	AGTGGAAGA	GAAAATCATC	GARCTGGCTG	GCTACCTGGA	TTCCTACATC	300
	CCAGAGCCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CTATCGAAGA	350
45	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAARGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAGGAC	450
	ACTGCTAAGT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTTCTGG	CTAAGCCAGG	CTCYATCAAG	600
50	CCGCACACCA	AGTTCGAATC	TGAAGTGATC	ATCCTGTCYA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACKACTGA	CGTGACCGGT	ACCATCGARC	TGCCAGAAGG	CGTTGAGATG	750
	GTAATGCCAG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCAAT	800
55	CGCAATGGAC	GATGGTCTGC	GTTC			824

2) INFORMATION FOR SEQ ID NO: 111

60 (i) SEQUENCE CHARACTERISTICS:

67

(A) LENGTH: 838 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: *Legionella micdadei*
 (B) STRAIN: ATCC 33218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111

	CGGAGCGATA	TTAGTAGTAT	CAGCAGCGGA	TGGCCCAATG	CCTCAAACGA	50
15	GAGAGCACAT	ACTYTTATCC	CGSCAGGTAG	GTGTTCCCTA	TATAGTAGTG	100
	TTCTTAAACA	AAGCTGACAT	GGTGGATGAT	GCGGAGTTAT	TAGAATTAGT	150
	TGAAATGGAA	GTACGCGAYT	TGTTGAGCAG	CTATGAATTT	CCAGGAGATG	200
	AGATCCCGAT	TGTAGTTGGT	TCAGCATTA	AAGCATTGGA	AGGCGATACG	250
	AGTGATATAG	GTGTACCAGC	GATTGAGAAG	TTAGTTGAGA	CGATGGATTC	300
20	TTATATACCT	GAGCCGGTAA	GAAACATCGA	TAAAAGTTTC	TTGTTACCGA	350
	TCGAAGACGT	GTTCTCAATA	TCTGGACGAG	GAACAGTAGT	AACAGGACGT	400
	ATCGAAAGCG	GGATCATCAA	AGTTGGTGAG	GAAGTCGAGA	TTGTTGGTAT	450
	ACGTGACACT	CAAAAGACGA	CATGCACAGG	CGTTGAAATG	TTCCGTAAAT	500
	TACTTGACGA	AGGTCGAGCT	GGAGACAACG	TTGGTATATT	GCTACGTGGT	550
25	ACGAAGCGGG	ATGAAGTTGA	ACGCGGACAA	GTATTAGCTA	AGCCGGGAAG	600
	CATTAAACCG	CATACTAAAT	TTGAAGCTGA	AGTGTATGTG	TTGTCAAAAG	650
	ATGAAGGTGG	ACGTCATACC	CCATTCTTTA	ACGGATATCG	GCCTCAATTT	700
	TACTTCAGGA	CCACAGACGT	AACTGGTTCT	TGTGATTTAC	CTGARGGTAT	750
	AGAAATGGTA	ATGCCAGGTG	ATAACGTCAA	GCTGATTGTT	AGCTTACACT	800
30	CACCGATTGC	TATGGACGAA	GGTTTGCGTT	TTGCAATC		838

2) INFORMATION FOR SEQ ID NO: 112

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 838 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
 (B) STRAIN: ATCC 33152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112

50	CGGAGCGATA	CTGGTTGTAT	CAGCAGCTGA	TGGTCCTATG	CCACAAACGA	50
	GGGAACACAT	TCTATTGTCT	CGCCAGGTAG	GTGTTCCATA	TATTGTTGTG	100
	TTCATGAACA	AAGCGGATAT	GGTTGATGAC	CCTGAGTTAT	TAGAGTTAGT	150
	GGAAATGGAA	GTGCGAGATT	TATTAAGCAG	TTACGATTTC	CCAGGGGATG	200
	ACATACCTAT	TGTTGTTGGT	TCAGCTTTGA	AAGCATTGGA	AGGTGAAGAC	250
55	AGTGATATAG	GCGTTAAGGC	TATTGAGAAA	TTGGTTGAAA	CAATGGATTC	300
	ATACATTCCCT	GAGCCAGTTA	GAAACATAGA	CAAGCCATTT	TTGTTGCCGA	350
	TTGAAGACGT	ATTTTCAATT	TCTGGACGCG	GAACAGTGGT	AACTGGTCGT	400
	GTAGAGAGTG	GAATTGTTAA	AGTTGGTGAG	GAAGTTGAAA	TTGTTGGAAT	450
	AAGAGACACC	CAAAAGACGA	CTTGTCAGGG	TGTTGAGATG	TTCCGTAAAT	500
60	TACTTGATGA	AGGTCGAGCT	GGTGATAACG	TTGGTGTGTT	ATTACGAGGT	550

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ACGAAGCGAG ATGAAGTGGA GCGTGGACAG GTATTGGCGA AGCCAGGAAC      600
CATCAAGCCA CACACCAAGT TTGAAGCAGA AGTGTATGTA TTATCCAAGG      650
AAGAAGGCGG ACGTCACACT CCATTCTTTA ATGGATACCG TCCACAATTC      700
TATTTTCAGAA CCACTGACGT GACAGGTACT TGTGACTTGC CATCAGGAGT      750
5  TGAAATGGTA ATGCCTGGAG ATAATGTGCA ATTAGTTGTT AGCTTGCATG      800
CTCCGATTGC GATGGATGAA GGTTTAAGAT TCGCAATT      838

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10 2) INFORMATION FOR SEQ ID NO: 113

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
15 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Leminorella grimontii
(B) STRAIN: ATCC 33999

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113

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25 GTGCAATCCT GGTAGTAGCA GCGACTGACG GCCCGATGCC TCAGACTCGC      50
GAGCACATCC TGCTGGGTCTG TCAGGTAGGC GTTCCGTACA TCATCGTATT      100
CCTGAACAAG TGCATATATGG TTGATGACGA AGAGCTGCTG GAGCTGGTTG      150
ARATGGAAGT TCGCGAACTG CTGTCTCAGT ACGACTTCCC GGGCGACGAC      200
30 ACTCCGGTAG TCCGCGGTTT AGCGCTGAAA GCGCTGGAAG GCGAAGCCGA      250
GTGGGAARCG AAAATCATCG AGCTGGCAGG CCMTCTGGAT ACTTATATCC      300
CAGAACCTGA GCGTGCGATT GACAAGCCGT TCCTGCTGCC KATCGAAGAC      350
GTATTCTCTA TCTCCGGCCG TGGTACCGTT GTTACCGGTC GTGTAGAGCG      400
CGGCATCATC AAAGTCGGTG AAGAAGTGGA AATCGTCCGT ATCAAAGATA      450
35 CCACCAAGAC CACCTGTACC GCGGTTGAAA TGTTCCGTAA GCTGCTGGAC      500
GAAGGCCGTG CGGGCGAGAA CGTGGGCGTT CTGCTGCGCG GTACCAAGCG      550
TGACGAAATC GAACGTGGTC AAGTTCTGGC CAAGCCGGGC ACCATCACTC      600
CTCACACCCA GTTCGTGTCA GAAGTGATA TCCTGAGCAA GGATGAAGGC      650
GGCCGTCATA CTCCGTTCTT CAAAGGCTAC CGTCCTCAGT TCTACTTCCG      700
40 TACGACTGAC GTGACAGGCA CCATCGAACT GCCGGAAGGC GTAGAGATGG      750
TAATGCCAGG CGACAACATT CAGATGACCG TAAGTCTGAT TCGCGCCGATC      800
GCAATGGACG AAGGTCTGCG CTTCGCAA      828

```

45

2) INFORMATION FOR SEQ ID NO: 114

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 826 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Leminorella richardii
(B) STRAIN: ATCC 33998

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60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114

	GCTATCCTGG	TTGTTGCTGC	GA CTGACGGC	CCAATGCCTC	AGACTCGTGA	50
	GCACATCCTG	CTGGGTCGCC	AGGTAGGCGT	TCCTTACATC	ATCGTGTTCC	100
	TGAACAAGTG	CGACATGGTT	GATGACGAAG	AGCTGCTGGA	ACTGGTAGAA	150
5	ATGGAAGTTC	GTGAACTTCT	GTCTCAATAC	GACTTCCCGG	GCGACGATAC	200
	GCCGGTTGTT	CGCGGTTGAG	CGCTGAAAGC	GCTGGAAGGT	GACGCGYAGT	250
	GGGAARCGAA	AATCATTGAA	CTGGCGGAAT	CCTTRGATAC	TTAYATTCCA	300
	GAGCCAGAGC	GTGCGATTGA	CAAGCCGTTT	CTGCTGCCTA	TCGAAGACGT	350
	TTTCTCTATC	TCTGGCCCGT	GTACTGTAGT	CACCGGTCGT	GTAGAGCGCG	400
10	GCATCATCAA	AGTTGGTGAA	GAAGTGGAAA	TCGTGGGAAT	CAAAGACACC	450
	ACCAAGACCA	CCTGTACTGG	CGTTGAAATG	TTCCGTAAGC	TGCTGGACGA	500
	AGGCCGTGCA	GGTGAGAACG	TTGGTGTTCT	GCTGCGYGGT	ACTAAGCGTG	550
	ACGAAATCGA	ACGTGGTCAG	GTACTGGCTA	AGCCAGGCAC	CATCACTCCT	600
	CACACGAAT	TCGTGTCAGA	AGTGTATATC	CTGAGCAAGG	ATGAAGCGCG	650
15	YCGTCATACT	CCGTTCTTCA	AAGGCTACCG	TCCTCAGTTC	TACTTCCGTA	700
	CGACTGACGT	GACCGGCACC	ATCGAACTGC	CAGAAGGCGT	AGAGATGGTA	750
	ATGCCAGGCG	ATAACATCCA	GATGGTAGTT	ACGCTGATTG	CCCCAATCGC	800
	GATGGACGAA	GGTCTGCGCT	TCGCAA			826
20						

2) INFORMATION FOR SEQ ID NO: 115

- (i) SEQUENCE CHARACTERISTICS:
- 25 (A) LENGTH: 843 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Leptospira interrogans*
(B) STRAIN: ATCC 23581
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115

	TGCGGCGATT	CTTG TAGTAT	CCGCAACTGA	CGGACCTATG	CCACAAACAA	50
	AAGAACATAT	CCTTCTTGCT	CGTCAGGTAG	GTGTTCCATA	TGTAATTGTA	100
40	TTCAATTAACA	AAGCAGATAT	GCTTGCTGCT	GACGAAAGAG	CAGAAATGAT	150
	CGAAATGGTT	GAGATGGACG	TTCGTGAAC	TCTCAATAAG	TATAGCTTCC	200
	CAGGAGATAC	AATCTCTATC	GTTCAATGTT	CTGCGGTAAA	AGCACTTGAG	250
	GGCGATGAAT	CTGAAATTGG	GATGCCTGCA	ATTCTCAAAT	TGATGGAAGC	300
	TCTGGATACT	TTCGTTCCAA	ATCCAAAACG	TGTAATCGAC	AAACCTTTCC	350
45	TTATGCCAGT	AGAAGACGTT	TTCTCGATCA	CTGGTCTGTT	AACTGTTGCA	400
	ACTGGAAGAG	TGGAACAAGG	TGTTTTGAAA	GTGAACGACG	AAGTTGAAAT	450
	TATCGGTATC	CGCCCAACAA	CAAAAACGTG	TGTTACCGGT	ATCGAAATGT	500
	TCAGAAAAC	TCTCGATCAA	GCGGAAGCTG	GCGACAACAT	CGGCGCTCTT	550
	CTTCGTGGAA	CTAAAAAAGA	AGAAATCGAA	AGAGGGCAAG	TTCTTGCGAA	600
50	GCCAGGTTCT	ATCACTCCTC	ACAAAAAGTT	TGCCGCTGAG	GTGTATGTAT	650
	TAATAAGGA	TGAAGGCGGA	CGTCATACT	CGTTTATCAA	TAATAACCGT	700
	CCTCAGTTTT	ACTTTAGAAC	AACGACGTA	ACCGGAGTTT	GTAACCTTCC	750
	TAATGGTGTC	GAAATGGTTA	TGCCTGGTGA	TAACGTTTCT	TTGACGGTTG	800
55	AATTGATTAG	CCCGATCGCA	ATGGACAAGG	GTCTTAAGTT	CGC	843

2) INFORMATION FOR SEQ ID NO: 116

- 60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Megamonas hypermegale*
 (B) STRAIN: ATCC 25560

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116

	CGGTGCTATC	CTCGTTGTTA	GTGCTGCTGA	TGGTCCTATG	CCTCAGACTC	50
15	GTGAACACAT	CCTTCTCGCT	CGTCAGGTTG	GTGTTCCAGC	TATCGTTGTA	100
	TTCCTCAACA	AAGCTGACCA	GGTTGATGAC	CCTGAACTTC	TCGAACTTGT	150
	TGAAATGGAA	GTTCTGTAAC	TTCTTTCCAG	CTATGACTTC	CCAGGCGATG	200
	ACGTTCCAGT	AATCACTGGT	TCCGCTCTTC	AGGCTCTCGA	AGGCGACGAA	250
	GAAGCTAAAA	AGAAAATTCT	TGAATTAATG	GATGCTGTTG	ATGATTACAT	300
20	CCCAACTCCA	ACACGTGACA	CTGATAAACC	TTTCTTAATG	CCAGTTGAAG	350
	ACGTATTAC	AATTACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGCGAAC	TTAAACTTGG	TGACAGCGTT	GAAATCGTTG	GTCCTTCCGA	450
	TGAAAAGAAA	TCCACTACTG	TAAC TGGTAT	CGAAATGTTC	CGCAAAATGC	500
	TTGATAGCGC	TGTTGCTGGT	GATAACATCG	GTGCACTTCT	TCGTGGTATT	550
25	GACCGTAAAG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CTGGCACAAT	600
	TCATCCACAC	AAAAAATTCA	AAGCTCAGGT	TTACGTATTA	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCTCCA	ACTATCGTCC	ACAGTTCTAT	700
	TTCCGTACTA	CTGACGTTAC	TGGTGTGTTA	ACTCTTCCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACATTGAAAT	GAGCATCGAA	CTCATCACTC	800
30	CAATCGCTAT	TGAAAAGGT	CTTCGCTTCG	CT		832

2) INFORMATION FOR SEQ ID NO: 117

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mitsuokella multacida*
 (B) STRAIN: ATCC 27723

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117

50	TGGTGCTATC	CTCGTCGTTT	CCGCTGCTGA	TGGCCCCGATG	CCGCAGACGC	50
	GTGAGACACAT	CCTGCTCGCT	CGCCAGGTCG	GTGTTCCGGC	AATCGTTGTC	100
	TTCCTCAACA	AGTTGACCA	GGTTGACGAT	CCGGAGCTCC	TCGAGCTCGT	150
	CGAGATGGAA	GTTGCGGAGC	TGCTCTCCAG	CTACGACTTC	CCGGGCGATG	200
	ACATCCCTGT	AATCGCTGGT	TCCGCTCTGA	AGGCCCTCGA	AGGCGACGAA	250
55	GAGCAGAAGA	AGAACATCCT	CAAGCTCATG	GAAGCTGTCTG	ATGAGTACAT	300
	CCCAGCGCCG	GTCCGCGACA	ACGCTAAGCC	GTTCTGATG	CCGGTCGAGG	350
	ATGTCTTCAC	GATCACGGGC	CGTGGTACGG	TTGCAACGGG	CCGCGTTGAG	400
	CGTGGTGAGC	TCAAGATGAA	CGATACGGTT	GAGATCGTTG	GTCTGCAGGA	450
	CGAGCCGCGT	CAGACGGTTG	TCACGGGCAT	CGAGATGTTC	CGCAAGATGC	500
60	TTGATTTTCG	TGAGGCTGGC	GATAACATCG	GTGCTCTGCT	CCGTGGTATC	550

GACCGCAAGG AGATCGAGCG TGGCCAGGTT CTCGCAAAGC CGGGCACGAT 600
 TCATCCGCAC ACGAAGTTCA AGGCTCAGGT CTATGTCCTG ACGAAAGAAG 650
 AAGGCGGCCG TCATACGCCG TTCTTCACGA ACTATCGCCC GCAGTTCTAC 700
 TTCCGCACGA CGGACGTAAC TGGCGTAGTC AAAGTGGCCG AAGGCACGGA 750
 5 GATGGTTATG CCTGGCGATA ACGTCGAGAT GGAAGTTGAG CTCATCACCC 800
 CGATCGCTAT CGAGAAGGGC 820

10 2) INFORMATION FOR SEQ ID NO: 118

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mobiluncus curtisii* subsp. *holmesii*
 (B) STRAIN: ATCC 35242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118

25 CGGCGCTATC CTCGTGGTGG CTGCTACTGA CGGTCCGATG GCTCAGACCA 50
 AGGAACACAT CCTGTTGGCT AAGCAGGTTG GCGTGCCCTC CATCCTGGTC 100
 GCTCTGAACA AGTGCGATTG TTCCGATGTG GACGAAGACA TGCTCGAAAT 150
 CGTCGAGGAC GAAATCCGCG ATGACCTGGA GAAGCAGGGC TTCGATCGTG 200
 30 ACTGCCCCGAT TATCCACGTT TCCGCTCTGA AGGCCCTGGA AGGCGACCCC 250
 GAGTGGACCA AGAAGATTGA AGAGCTCATG GAAGCGGTGCG ATACCTACAT 300
 TCCTGAGCCT GTTCGTGACC TCGACAAGCC GTTCTTGATG CCTATCGAAG 350
 ACGTCTTCAC CATTACTGGT CGCGGTACCG TAGTGACCGG TCGTGTGGAA 400
 CGCGGCAAGC TACCGTTGAA CGCCGAAGTG GAAATCGTAG GTATTCTGCC 450
 35 TACGCAAAAG ACCACCGTTA CCGGTATCGA AATGTTCCAC AAGTCCATGG 500
 ACGAAGCCTA CGCCGCGCAG AACTGTGGTC TGTGCTGCG TGGCACCAAG 550
 CGTGAGGACG TTGAGCGCGG TCAGGTTGTC TGCATTCTG GCTCCGTGAC 600
 CCCGCACACC AAGTTCGAGG GCAAGGTCTA CATCTTGAAG AAGGACGAAG 650
 GTGGACGTCA CAAGTCGTTT TACGACGGCT ACCGCCCCGA GTTCTTCTTC 700
 40 CGCACCACCG ACGTGACCGG TGTTATTCAC CTGCCCCGAG GCACCGAAAT 750
 GGTTATGCCT GCGGACACCA CCGAAATTAG CGTTGAGCTG ATTCAGCCTA 800
 TCGCTATGGA GGAAGGTCTC GGCTTCGCTA 831

45

2) INFORMATION FOR SEQ ID NO: 119

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moellerella wisconsensis*
 (B) STRAIN: ATCC 35017

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119


```

GGTGCAATTC TGGTTGTTGC TGCAACTGAT GGCCCTATGC CACAGACTCG      50
TGAGCACATC CTGTTAGGTC GTCAGGTTGG CGTTCCATAC ATCATCGTTT      100
TCCTGAACAA ATGTGACATG GTAGACGACG AAGAGCTGTT AGAACTGGTT      150
5  GAAATGGAAG TCCGTGAGCT GCTGTCTCAG TACGATTTCC CAGGCGATGA      200
  CACTCCAGTA ATCCGTGGTT CAGCGCTGAA AGCTCTGGAA GGCGAAGCTG      250
  AGTGGGAAGC TAAATCATT GAACTGGCAG AAGCACTGGA TTCTTATATC      300
  CCAGAGCCAG AGCGTGACAT TGATAAGCCA TTCCTGTTAC CAATCGAAGA      350
  CGTATTCTCA ATTTCAGGCC GTGGTACAGT TGTTACTGGT CGTGTTGAGC      400
10 GTGGTATCGT TAAAGTCGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAT      450
  ACCGTGAAAA CAACATGTAC TGGCGTTGAA ATGTTCCGTA AACTGCTGGA      500
  CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTACTAAAC      550
  GTGATGATAT CGAACGTGGT CAAGTATTGG CTAAACCAGG TTCAATCACT      600
  CCGCATACAA CTTTCGAATC AGAAGTTTAC ATCCTGAGCA AAGATGAAG      650
15 TGGCCGTCAT ACTCCATTCT TCAAAGGTTA CCGTCCACAG TTCTACTTCC      700
  GTACAACGTGA CGTAACCGGT ACTATCGAAC TGCCAGAAGG CGTTGAGATG      750
  GTAATGCCAG GTGATAACAT CAAAATGATC GTTACTCTGA TCCACCCAAT      800
  TGCAATGGAT GCAGGTCTGC GTTTTT      825

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20

2) INFORMATION FOR SEQ ID NO:120

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      (i) SEQUENCE CHARACTERISTICS:
25  (A) LENGTH: 827 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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      (A) ORGANISM: Branhamella catarrhalis
      (B) STRAIN: ATCC 43628

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120

```

TGGTGCTATC TTGGTTGTTT CTGCAACTGA TGGTCCTATG CCACAAACTC      50
GTGAGCATAT CCTACTATCT CGTCAGGTTG GTGTACCATA CATCATGGTA      100
40 TTCATGAACA AGTGCGATAT GGTTGATGAT GAAGAGCTAC TAGAATTGGT      150
  TGAAATGGAA GTTCGTGAAC TTCTATCTGA CTATGATTTC CCTGGTGATG      200
  ATACCCCAAT CATCAAAGGT TCAGCACTAG AAGCATTGAA TGGTTCTGAT      250
  GGTAAATATG GCGAGCCTGC AGTTCTAGAA CTGCTAGACA CACTAGACAG      300
  CTATATCCCA GAGCCTGAGC GTGATATCGA TAAGTCATTC TTGATGCCAA      350
45 TTGAAGATGT CTTCTCGATC TCAGGTCGTG GTACAGTTGT GACTGGTCGT      400
  GTTGAATCAG GTATTATTAA AGTTGGTGAT GAAATTGAAA TCATCGGTAT      450
  CAAACCAACT GCTAAAACCA CCTGTACTGG TGTTGAAATG TTCCGTAAAC      500
  TGTTAGACGA AGGTCGTGCA GGTGAGAACT GTGGTATCTT GTTGCCTGGT      550
  ACTAAGCGTG AAGAAGTTCA ACGCGGTCAA GACTTGCAA AACCAGGTTC      600
50 AATCACCCCA CATACTAAGT TTGATGCTGA AGTTTATGTA CTGTCAAAG      650
  AAGAAGGTGG TCGTCACACC CCATTCTTAA ATGGCTATCG CCCACAGTTC      700
  TACTTCCGTA CCACAGATGT GACTGGTGCC ATCACTCTAC AAGAAGGTAC      750
  CGAAATGGTT ATGCCTGGTG ACAATGTTGA GATGAGTGTT GAGCTTATCC      800
  ACCCAATCGC CAGGATAAAG GTCTACG      827

```

55

2) INFORMATION FOR SEQ ID NO: 121

60 (i) SEQUENCE CHARACTERISTICS:

73

(A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Morganella morganii* subsp. *morganii*
 (B) STRAIN: ATCC 25830

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121

	CGGCGCTATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACCC	50
15	GTGAGCACAT	CCTGTTAGGT	CGTCAGGTTG	GCGTTCCTTA	CATCATCGTA	100
	TTCCTGAACA	AATGTGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCTGGCGACG	200
	ACACGCCAAT	CGTTCGCGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAGCCA	250
	GAGTGGGAAG	CTAARATCGT	TGAAGTGGCA	GGTTTCCTGG	ATTCTTACAT	300
20	CCCTGAGCCA	GAGCGTGCAA	TTGACAAGCC	GTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	AATCTCCGGC	CGTGGTACCG	TTGTTACCGG	TCGTGTTGAG	400
	CGCGGTATCA	TCAAGGTTGG	TGAGGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	TACTGCGAAA	ACCACCTGTA	CCGGTGTGTA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCMGGTGAG	AACGTCGGTG	TTCTGCTGCG	TGGTACCAAG	550
25	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCTAAACCAG	GTTCAATCAA	600
	ACCACAYACC	AAATTTGAAT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGGYT	ACCGTCCACA	GTTCTACTTC	700
	CGTACCACAG	ACGTAACAGG	TACTATCGAA	CTGCCGGAAG	GCGTTGAAAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGAT	CGTCACCCTG	ATCCACCCAA	800
30	TCGCAA					806

2) INFORMATION FOR SEQ ID NO: 122

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*
 (B) STRAIN: TB 299

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122

50	GGTGCGATCC	TGGTGGTCGC	CGCCACCGAC	GGCCCGATGC	CCCAGACCCG	50
	CGAGCACGTT	CTGCTGGCGC	GTCAAGTGGG	TGTGCCCTAC	ATCCTGGTAG	100
	CGCTGAACAA	GGCCGACGCA	GTTGACGACG	AGGAGCTGCT	CGAACTCGTC	150
	GAGATGGAGG	TCCGCGAGCT	GCTGGCTGCC	CAGGAATTCT	ACGAGGACGC	200
	CCCGGTTGTG	CGGGTCTCGG	CGCTCAAGGC	GCTCGAGGGT	GACGCGAAGT	250
55	GGGTTGCCTC	TGTCGAGGAA	CTGATGAACG	CGGTCGACGA	GTCGATTCCG	300
	GACCCGGTCC	GCGAGACCGA	CAAGCCGTTC	CTGATGCCGG	TCGAGGACGT	350
	CTTCACCATT	ACCGGCCGCG	GAACCGTGGT	CACCGGACGT	GTGGAGCGCG	400
	GCGTGATCAA	CGTGAACGAG	GAAGTTGAGA	TCGTCGGCAT	TCGCCCATCG	450
	ACCACCAAGA	CCACCGTCAC	CGGTGTGGAG	ATGTTCCGCA	AGCTGCTCGA	500
60	CCAGGGCCAG	GCGGGCGACA	ACGTTGGTTT	GCTGCTGCGG	GGCGTCAAGC	550

	GCGAGGACGT	CGAGCGTGGC	CAGGTTGTCA	CCAAGCCCGG	CACCACCACG	600
	CCGCACACCG	AGTTCGAAGG	CCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	650
	CGGCCGGCAC	ACGCCGTTCT	TCAACAATA	CCGTCCGCAG	TTCTACTTCC	700
	GCACCACCGA	CGTGACCGGT	GTGGTGACAC	TGCCGGAGGG	CACCGAGATG	750
5	GTGATGCCCC	GTGACAACAC	CAACATCTCG	GTGAAGTTGA	TCCAGCCCCG	800
	CGCCATGGAC	GAAGGTCTGC	GTTTC			825

10 2) INFORMATION FOR SEQ ID NO: 123

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria cinerea*
 (B) STRAIN: ATCC 14685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123

25	CGGTGCGATC	TTGGTATGTT	CCGCAGCTGA	CGGTCCTATG	CCGCAAACCTC	50
	GCGAACACAT	CCTGTTGGCC	CGCCAAGTAG	GTGTACCTTA	CATCATCGTG	100
	TTCATGAACA	AATGCGACAT	GGTTGACGAT	GCCGAGCTGT	TGGAGCTGGT	150
	TGAAATGGAA	ATCCGTGACT	TGCTGTCAAG	CTACGACTTC	CCAGGTGACG	200
30	ACTGCCCCGAT	CGTACAAGGT	TCTGCACTGA	AAGCCTTGGA	AGGCGACGCA	250
	GCTTACGAAG	AAAAAATCTT	CGAATTGGCT	GCTGCATTGG	ACAGCTACAT	300
	CCCAACACCT	GAGCGTGCAG	TGGACAAACC	TTTCTTGTTG	CCTATCGAAG	350
	ACGTATTCTC	TATTTCCGGT	CGCGGTACAG	TAGTAACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCCACGTTGG	TGACGAGATC	GAAATCGTAG	GTCTGAAAGA	450
35	AACTCAAAAA	ACCACTTGTA	CCGGTGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCA	AGCTGGTGAC	AACGTAGGTG	TATTGCTGCG	TGGTACTAAA	550
	CGTGAAGACG	TAGAGCGTGG	TCAAGTATTG	GCTAAACCGG	GTACTATCAC	600
	TCCTCACACC	AAGTTCAAAG	CAGAAGTATA	CGTACTGAGC	AAAGAAGAGG	650
	GTGGTCGTCA	CACTCCGTTC	TTCGCTAACT	ACCGTCCACA	ATTCTACTTC	700
40	CGTACTACCG	ACGTAACCGG	CGCGGTTACT	TTGGAAGAAG	GTGTAGAAAT	750
	GGTAATGCCG	GGTGAGAACG	TAACCATTAC	TGTAGAAGTG	ATTGCGCCTA	800
	TCGCTA					806

45

2) INFORMATION FOR SEQ ID NO: 124

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria elongata* subsp. *elongata*
 (B) STRAIN: ATCC 25295

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124

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CGGCGCAATC TTGGTATGTT CCGCTGCTGA CCGTCCTATG CCGCAAACCTC 50
GCGAACACAT CCTGTTGGCC CGCCAAGTAG GCGTACCTTA CATCATCGTG 100
TTCATGAATA AATGCGACAT GGTGAYGAT GCCGAACCTG TGGAACTGGT 150
5 TGAAATGGAA ATCCGTGACT TGCTGTCAAG CTACGACTTC CCAGGCGACG 200
ACTGCCCCGAT CGTACAAGGT TCCGCACTGA AAGCCTTGGA AGGCGACGCA 250
GCTTACGAAG AAAAAATCTT CGAACTGGCT GCTGCATTGG ACAGCTACAT 300
CCCGACACCT GAGCGTGCCG TGGACAAACC GTTCCTGTTG CCTATCGAAG 350
ACGTATTCTC TATCTCCGGC CGTGGTACAG TAGTAACCGG TCGTGTAGAG 400
10 CGCGGTATCA TCCACGTCGG TGACGAGATC GAAATCGTAG GTCTGAAAGA 450
AACCCAAAAA ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAAGTGTCTG 500
ACGAAGGTCA AGCAGGTGAC AACGTAGGCG TATTGCTGCG CCGTACCAAA 550
CGTGAAGAAG TGAACGCGG TCAAGTATTG GCTAAACCGG GTACCATCAC 600
TCCTCACACC AAATTCAAAG CAGAAGTTTA CGTATTGAGC AAAGAAGAGG 650
15 GTGGTCGTC TACTCCGTTT TCGCTAACT ACCGTCCACA ATTCTACTTC 700
CGTACTACCG ACGTAACCGG TCGGGTACT TTGGAAGAAG GTGTAGAAAT 750
GGTTATGCCT GGTGAGAACG TGGCCATCAC TGTAAGACTG ATTGCACCTA 800
TCGCTATGGA AGAAGGTCTG CG 822

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20

2) INFORMATION FOR SEQ ID NO: 125

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25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 820 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Neisseria flavescens
        (B) STRAIN: ATCC 13120

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125

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CGGCGCGACT TGGTATGTTT CGCAGCTGAC GGTCTTATGC CGCAAACCCG 50
CGAACACATC CTGTTGGCTC GCCAAGTAGG TGTACCTTAC ATCATCGTAT 100
40 TCATGAACAA ATGCGACATG GTAGACGATG CCGAGCTGTT GGAAGTGGTT 150
GAAATGGAAA TTCGTGACTT GTTGTCAAGC TACGACTTCC CAGGCGACGA 200
CTGCCCAATC GTACAAGGTT CTGCACTGAA AGCTTTGGAA GGTGATGCTG 250
CTTACGAAGA AAAAAATCTT GAATTGGCTG CTGCCTTGGA CAGCTACATC 300
CCAACACCTG AGCGTGCTGT GGACAAACCT TTCTTGTTGC CTATCGAAGA 350
45 CGTATTCTCT ATCTCTGGTC GTGGTACAGT AGTAACCGGT CCGGTAGAGC 400
GCGGTATCAT CCACGTTGGT GACGAGATCG AAATCGTAGG TCTGAAAGAA 450
ACTCAAAAAA CCACTTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
CGAAGGTCAA GCAGGTGACA ACGTAGGCGT ATTGCTGCGT GGTACTAAAC 550
GTGAAGACGT AGAGCGTGGT CAAGTATTGG CTAAACCAGG TACCATCACT 600
50 CCTCACACCA AATTCAAAGC AGAAGTATAC GTACTGAGCA AAGAAGAGGG 650
TGGTCGTCAC ACTCCATTTT TCGCTAACTA CCGTCCACAA TTCTACTTCC 700
GTACTACCGA CGTAAGTGGT GCGTTACTT TGGGAAGAAG CGTAGAAATG 750
GTAATGCCAG GTGAGAACGT AACCATTACT GTAGAAGTGA TTGCGCCAAT 800
CGCTATGGAA GAAGTCTGCG 822

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2) INFORMATION FOR SEQ ID NO: 126

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60 (i) SEQUENCE CHARACTERISTICS:

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76

(A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*
 (B) STRAIN: ATCC 49226

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126

15	GGTGCAATCC	TGGTATGTTC	TGCTGCCGAC	GGCCCTATGC	CGCAAACCCG	50
	CGAACACATC	CTGCTGGCCC	GTCAAGTAGG	CGTACCTTAC	ATCATCGTGT	100
	TCATGAACAA	ATGCGACATG	GTCGACGATG	CCGAGCTGTT	GGAAGTGGTT	150
	GAAATGGAAA	TCCGCGACCT	GCTGTCCAGC	TACGACTTCC	CCGGCGACGA	200
	CTGCCCGATC	GTACAAGGTT	CCGCACTGAA	AGCCTTGGAA	GGCGATGCCG	250
	CTTACGAAGA	AAAAATCTTC	GAAGTGGCTA	CCGCATTGGA	CAGCTACATC	300
20	CCGACTCCCG	AGCGTGCCGT	GGACAAACCA	TTCCTGCTGC	CTATCGAAGA	350
	CGTGTTCTCC	ATTTCCGGCC	GCGGTACCGT	AGTCACCGGC	CGTGTAGAGC	400
	GAGGTATCAT	CCACGTTGGT	GACGAGATTG	AAATCGTCGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAG	GCGGGCGACA	ACGTAGGCGT	ATTGCTGCGC	GGTACCAAAC	550
25	GTGAAGACGT	AGAACGCGGT	CAGGTATTGG	CCAAACCGGG	TACTATCACT	600
	CCTCACACCA	AGTTCAAAGC	AGAAGTGTAC	GTATTGAGCA	AAGAAGAGGG	650
	CGGCCGCCAT	ACCCCGTTTT	TCGCCAACTA	CCGTCCCCAA	TTCTACTTCC	700
	GTACCACTGA	CGTAACCGGC	GCGGTTACTT	TGGAAAAAGG	TGTGGAAATG	750
	GTAATGCCGG	GTGAGAACGT	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	800
30	CGCTATGGAA	GAAGGTCTGC	GCTTTGCGAT			830

2) INFORMATION FOR SEQ ID NO: 127

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria lactamica*
 (B) STRAIN: ATCC 23970

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127

50	CGGCGCAATC	TTGGTATGTT	CCGCCGCCGA	CGGCCCTATG	CCGCAAACCC	50
	GCGAACACAT	TCTGTTGGCC	CGCCAAGTAG	GTGTACCTTA	CATCATCGTA	100
	TTCATGAACA	AATGCGATAT	GGTCGACGAT	GCCGAGCTGT	TGGAAGTGGT	150
	TGAAATGGAA	ATCCGCGACC	TGCTGTCAAG	CTACGACTTC	CCAGGCGACG	200
	ACTGCCCAAT	CGTACAAGGT	TCCGCACTGA	AAGCTTTGGA	AGGCGATGCC	250
55	GCTTACGAAG	AAAAAATCTT	CGAACTGGCT	GCCGCATTGG	ACAGCTACAT	300
	CCCGACTCCC	GAGCGTGCCG	TGGACAAACC	GTTCTTGCTG	CCTATCGAAG	350
	ACGTATTCTC	CATCTCCGGC	CGCGGTACGG	TAGTAACCGG	CCGTGTAGAG	400
	CGCGGTGTCA	TCCACGTTGG	CGACGAGATC	GAAATCGTCG	GTCTGAAAGA	450
	AACCCAAAAA	ACCACCTGTA	CCGGTGTCGA	GATGTTCCGC	AAACTGCTGG	500
60	ACGAAGGTCA	GGCAGGCGAC	AACGTAGGCG	TATTGCTGCG	CGGTACCAAA	550

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CGTGAAGAAG TGGAACGCGG TCAGGTATTA GCCAAACCGG GTACCATCAC      600
TCCGCACACC AAGTTCAAAG CAGAAGTGTA TGTATTGAGC AAAGAAGAGG      650
GCGGTCGTCA CACTCCGTTT TCGCCAACT ACCGTCCGCA ATTCTACTTC      700
CGTACCACCG ACGTAACCGG CGCGGTTACT TTGGAAGAAG GCGTGGAAT      750
5  GGTAAATGCC GGTGAGAACG TAACCATTAC TGTAGAACTG ATTGCGCCTA      800
   TCGCTATGGA AGAAGG      816

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10 2) INFORMATION FOR SEQ ID NO: 128

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*
 (B) STRAIN: ATCC 13077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128

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25 CCGTGCAATC CTGGTATGTT CCGCAGCCGA CCGTCCTATG CCGCAAACCC      50
   GCGAACACAT CCTGCTGGCC CGTCAAGTAG GCGTACCTTA CATCATCGTG      100
   TTCATGAACA AATGCGACAT GGTCGACGAT GCCGAGCTGT TGGAAGTGGT      150
   TGAAATGGAA ATCCGCGACC TGCTGTCCAG CTACGACTTC CCCGCGGACG      200
30 ACTGCCCCGAT CGTACAAGGT TCCGCACTGA AAGCCTTGGA AGGCGATGCC      250
   GCTTACGAAG AAAAAATCTT CGAATTGGCT GCTGCATTGG ACAGCTACAT      300
   CCCGACTCCC GAGCGTGCCG TGGACAAACC TTTCTTGTTG CCTATCGAAG      350
   ACGTATTCTC TATTTCCGGT CGTGGTACAG TAGTAACCGG TCGTGTAGAG      400
   CGCGGTATCA TCCACGTCGG TGACGAGATC GAAATCGTCG GTCTGAAAGA      450
35 AACTCAAAAA ACCACTTGTA CCGGTGTTGA AATGTTCCGC AACTGCTGG      500
   ACGAAGGTCA AGCAGGCGAC AACGTAGGCG TATTGCTGCG CGGTACCAAA      550
   CGTGAAGACG TAGAGCGTGG TCAAGTATTG GCTAAACCGG GTACAATCAC      600
   TCCTCACACC AAGTTCAAAG CAGAAGTATA CGTACTGAGC AAAGAAGAGG      650
   GCGGCCGCCA TACCCCGTTC TTCGCCAACT ACCGTCCCCA ATTCTACTTC      700
40 CGTACCACCG ACGTAACCGG CGCGGTTACT TTGGAAGAAG GTGTGGAAAT      750
   GGTAAATGCC GGCAGAGAACG TAACCATCAC CGTAGAACTG ATTGCGCCTA      800
   TCGCTATGGA AGAAGGTTTG CGCTTTGCGA T

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831

45

2) INFORMATION FOR SEQ ID NO: 129

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 815 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria mucosa*
 (B) STRAIN: ATCC 19696

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129

CGGCGCAATC TTGGTATGTT CTGCTGCTGAC CGGTCCTATG CCGCAAACCC 50
 GYGAACACAT CCTGTTGGCC CGTCAAGTAG GYGTACCTTA CATCATCGTG 100
 TTCATGAACA AATGCGACAT GGTTGACGAT GCCGAAYTGT TGGAAGTGGT 150
 5 TGAAATGGAA ATCCGTGACT TGCTGTCAAG CTACGACTTC CCTGGYGACG 200
 ACTGCCCGAT TGTACAAGGT TCTGCACTGA AAGCCTTGA AGGCGATGCC 250
 GCTTACGAAG AAAAAATCTT CGAACTGGCT GCCGCATTGG ACAGCTACAT 300
 CCCGACTCCC GAGCGTGCCG TAGACAAACC GTTCCTGTTG CCTATCGAAG 350
 ACGTATTCTC CATCTCCGTG CGTGGTACAG TAGTAACCGG CCGTGTAGAG 400
 10 CGCGGTGTTA TCCACGTTGG TGACGAGATC GAAATCGTAG GTCTGAAAGA 450
 AACCCAAAAA ACCACATGTA CCGGTGTTGA AATGTTCCGC AAAGTCTGCTGG 500
 ACGAAGGTCA AGCCGGTGAC AACGTAGGCG TATTGCTGCG CCGTACCAA 550
 CGTGAAGAAG TGGAACGCGG TCAAGTATTG GCTAAACCGG GTACCATCAC 600
 TCCGCACACC AAATTCAAAG CAGAAGTGTA CGTATTGAGC AAAGAAGAGG 650
 15 GTGGTCGTCA TACTCCGTTC TTCGCTAACT ACCGTCCTCA ATTCTACTTC 700
 CGTACTACCG ACGTAACCGG TCGGTTACT TTGGAAGAAG GTGTAGAAAT 750
 GGTTATGCCT GGTGAGAAAG TAGCCATYAC TGTAGAACTG ATTGCGCCTA 800
 TYGCTATGGA AGAAG 815

20

2) INFORMATION FOR SEQ ID NO: 130

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Neisseria sicca*
 (B) STRAIN: ATCC 9913

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130

GGCGCAATCT TGGTATGTTT CGCTGCTGAC GGTCCTATGC CGCAAACCCG 50
 CGAACACATC CTGTTGGCCC GCCAAGTAGG CGTACCTTAC ATCATCGTGT 100
 40 TCATGAACAA ATGCGACATG GTTGACGATG CCGAGCTGTT GGAAGTGGTT 150
 GAAATGGAAA TCCGTGACTT GCTGTCAAGC TACGACTTCC CTGGTGACGA 200
 CTGCCCCGATC GTACAAGGTT CTGCACTGAA AGCCTTGGA GGCGACGCCG 250
 CTTACGAAGA AAAAATCTTC GAACTGGCTG CTGCATTGGA CAGCTACATC 300
 CCGACTCCTG AGCGTGCCGT GGACAAACCG TTCTGTTGC CTATTGAAGA 350
 45 CGTATTCTCC ATCTCCGGTC GCGGTACCGT AGTAACCGGC CGTGTAGAGC 400
 GCGGTGTTAT CCACGTTGGT GACGAGATTG AAATCGTAGG TCTGAAAGAA 450
 ACCCAAAAAA CCACTTGTAC CCGTGTGTA ATGTTCCGCA AACTGCTGGA 500
 CGAAGGTCAA GCCGGTGACA ACGTAGGCGT ATTGCTGCGC GGTACCAAAC 550
 GTGAAGAAGT GGAACGCGGT CAAGTATTGG CTAAACCGGG TACCATCACT 600
 50 CCTCACACTA AATTCAAAGC AGAAGTTTAC GTATTGAGTA AAGAAGAGGG 650
 TGGTCGTCAT ACTCCGTTCT TCGCTAACTA CCGTCCTCAA TTCTACTTCC 700
 GTACTACCGA CGTAACCGGC GCGGTTACTT TGGAAGAAGG TGTAAGAAATG 750
 GTTATGCCTG GTGAGAACGT AGCCATCACT GTAGAAGTGA TTGCACCGAT 800
 CGCTATGGAA GAAGGTCTGC GCTTTGCGA 829

55

2) INFORMATION FOR SEQ ID NO: 131

60 (i) SEQUENCE CHARACTERISTICS:

79

(A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria subflava*
 (B) STRAIN: ATCC 14221

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131

15	CGGCGCGACT	TGGTATGTTT	CGCAGCTGAT	GGTCCTATGC	CTCAAACCTCG	50
	CGAACACATC	CTGTTGGCTC	GCCAAGTAGG	TGTACCTTAC	ATCATCGTAT	100
	TCATGAACAA	ATGCGACATG	GTTGACGATG	CCGAGCTGTT	GGAAGTGGTT	150
	GAAATGGAAA	TCCGTGACCT	GTTGTCAAGC	TACGACTTCC	CAGGCGACGA	200
	CTGCCCAATC	GTACAAGGTT	CTGCACTGAA	AGCTTTGGAA	GGTGACGCTG	250
	GTTACGAAGA	GAAAATCTTC	GAATTGGCTG	CTGCTCTGGA	CAGCTACATC	300
20	CCAACACCTG	AGCGTGCTGT	GGACAAACCT	TTCTTGTTGC	CTATCGAAGA	350
	CGTATTCTCT	ATCTCTGGCC	GTGGTACAGT	AGTAACTGGT	CGTGTAGAGC	400
	GCGGTATCAT	CCACGTTGGT	GACGAGATCG	AAATCGTAGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACTTGTA	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAA	GCTGGTGACA	ACGTAGGCGT	ATTGCTGCGT	GGTACCAAAC	550
25	GTGAAGACGT	AGAGCGTGGT	CAAGTATTGG	CTAAACCAGG	TACCATTACT	600
	CCTCACACCA	AATTCAAAGC	AGAAGTATAC	GTACTGAGCA	AAGAAGAGGG	650
	TGGTCGTCAC	ACTCCATTCT	TCGCTAACTA	CCGTCCACAA	TTCTACTTCC	700
	GTACTACTGA	CGTAACTGGT	GCAGTTACTT	TGGAAGAAGG	CGTAGAAATG	750
	GTAATGCCAG	GTGAGAACGT	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	800
30	CGCTATGGAA	GAAG				814

2) INFORMATION FOR SEQ ID NO: 132

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria weaveri*
 (B) STRAIN: ATCC 51223

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132

50	GCCATCTTGG	TATGTTCTGC	TGCTGACGGT	CCTATGCCGC	AAACCCGTGA	50
	GCACATCCTG	TTGGCTCGTC	AAGTAGGTGT	ACCCTACATC	ATCGTATTCA	100
	TGAACAAATG	CGATATGGTT	GATGATGCAG	AGCTGCTGGA	ATTGGTAGAA	150
	ATGGAAATCC	GTGATCTGCT	GAGCAGCTAC	GATTTCCTTG	GCGATGATTG	200
	YCCAATCGTG	CAAGGTTCTG	CTTTGAAAGC	TTTGGAAGGT	GATGCCGCTT	250
55	ACGAAGAAAA	AATCTTTGAA	TTAGCTGCTG	CATTGGATAG	CTATATTCCA	300
	ACWCCTGAGC	GYGCTGTTGA	TAAACCATTC	CTGTTGCCGA	TTGAAGATGT	350
	ATTCTCAATT	TCAGGTCGTG	GTACAGTAGT	AACTGGTCGT	GTAAGACGCG	400
	GTATTATTCA	CGTAGGCGAT	GAAATTGAAA	TTGTAGGTTT	GAAAGARACY	450
	CAAAAACTA	CTTGTAACCG	CGTTGAAATG	TTCCGTAAAT	TGCTGGATSA	500
60	AGGTCAGGCT	GGTGATAACG	TAGGCGTATT	GTGCGTGGT	ACCAAACGTG	550

80

AAGACGTTGA GCGTGGTCAA GTATTGGCTA AGCCTGGTWC TATTACTCCG 600
 CAYACCAAAT TCAAAGCAGA RGTKTATGTW TTGAGYAAGG AAGAAGGCCG 650
 TCGTCATACT CCGTTCCTTCG CTAACATATCG TCCGCAATTC TATTTCCGTA 700
 CTACAGACGT TACCGGTGCK GTRACTTTAG AAGAAGGTGT GGAAATGGTA 750
 5 ATGCCTGGTG AGAAYGTTGC CATTACTGTW GARYTGATYG CTCCGATTGC 800
 KATGGAAGAA GGYTGCGT 818

10 2) INFORMATION FOR SEQ ID NO: 133

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: Genomic DNA

 20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Ochrobactrum anthropi*
 (B) STRAIN: ATCC 49188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133
 25 CGGCGCAATT CTGGTTGTTT CGGCCGCTGA CGGCCCGATG CCGCAGACCC 50
 GTGAGCACAT CCTGCTCGCT CGTCAGGTTG GCGTTCCGGC AATCGTCGTG 100
 TTCCTGAACA AGTGCGACCA GGTTGACGAT GCAGAACTGC TCGAACTGGT 150
 TGAAGTGGAA GTTCGCGAAC TTCTGTGCGAA ATACGATTTC CCGGGCGACG 200
 30 AAGTTCCGAT CATCAAGGGC TCGGCTCTTG CTGCTCTGGA AGATTCTTCG 250
 AAGGAAGTGG GCGAAGACGC CGTTCGTTCG CTGATGGCCG CTGTTGACGA 300
 CTACATTCCG ACCCCGGAAC GTCCGATCGA CCAGCCGTTT CTGATGCCGA 350
 TCGAAGACGT TTTCTCGATC TCGGGCCGTG GTACGGTTGT GACGGGTGCG 400
 GTTGAGCGCG GTATCGTCAA GGTTGGTGAA GAAGTTGAAA TCGTCGGCAT 450
 35 CAAGGCGACG GCGAAGACGA CGGTAACCGG CGTTGAAATG TTCCGCAAGC 500
 TGCTCGAYCA GGGCCAGGCT GGCGACAACA TCGGCGCTCT GATCCGCGGC 550
 GTTGGCCGTG AAGACGTTGA ACGCGGCCAG GTTCTCTGCA AGCCGGGTTT 600
 TGTGAAGCCG CACACCAAGT TCAAGGCAGA AGCCTACATT CTGACCAAGG 650
 ACGAAGGTGG CCGTCATACG CCGTTCCTTA CGAACTACCG TCCGCAGTTC 700
 40 TACTTCCGCA CGACGGACGT GACCGGTGTT GTCACGCTGC CGGAAGGCAC 750
 GGAAATGGTT ATGCCTGGCG ACAACGTGCG TATGGACGTC ACCCTGATCG 800
 TGCCGATCGC CATGGAAGAG AAGCTCCGCT TCGCTA 836

45 2) INFORMATION FOR SEQ ID NO: 134

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 805 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: Genomic DNA

 55 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Pantoea agglomerans*
 (B) STRAIN: ATCC 27155

 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134

5 CCTGGTTGTT GCTGCGACTG ATGGCCCAAT GCCACAGACC CGTGAGCACA 50
 TCCTGCTGGG TCGTCAGGTT GGC GTTCCTGAAC 100
 AAGTGTGACA TGGTTGATGA TGAAGAGCTG CTGGAAGTGG TAGAGATGGA 150
 AGTACGTGAC CTGCTGTCAC AGTACGACTT CCCAGGCGAT GACACCCCGA 200
 TCGTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGTTCC TGAGTGGGAA 250
 GCAAAAATCG TTGAGCTGGC TGAACACCTG GACAACTACA TCCCGGATCC 300
 AGTCCGTGCG ATCGACATGC CGTTCCTGCT GCCAATCGAA GACGTATTCT 350
 CAATCTCTGG CCGTGGTACC GTTGTTACCG GTCGTGTTGA GCGCGGCATC 400
 10 GTTAAAGTCG GCGACGAAGT TGAAATCGTG GGTATCAAAG ATACTGCGAA 450
 ATCAACCTGT ACCGGTGTGG AGATGTTCCG TAAGCTGCTG GACCAGGGTC 500
 AGGCAGGCGA AAAGTGTGGT GTTCTGCTGC GCGGTATCAA GCGTGAAGAC 550
 ATCCAGCGTG GCCAGGTTCT GGCTAAGCCA GGCTCAATCA AGCCGCACAC 600
 CCAAGTTCGAG TCAGAAAGTT ACGTTCTGTC TAAAGACGAA GGTGGCCGCC 650
 15 ATACTCCGTT CTTCAAAGGC TATCGTCCAC AGTTCTACTT CCGTACAACT 700
 GATGTAACCG GTTCAGTAGA GCTGCCAGAA GCGGTTGAGA TGGTCATGCC 750
 AGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCA ATCGCAATGG 800
 ACGAA 805

20

2) INFORMATION FOR SEQ ID NO: 135

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pantoea dispersa*
 (B) STRAIN: ATCC 14589

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135

40 CGCGATCCTG GTTGGTTGCTG CGACTGATGG CCCAATGCCT CAGACCCGTG 50
 AGCACATCCT GCTGGGCCGT CAGGTTGGCG TTCCTTACAT CATCGTGTTT 100
 CTGAACAAGT GTGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA 150
 GATGGAAGTT CGCGATCTGC TGTCTCAGTA CGACTTCCCA GGCGACGATA 200

 45 CCCCATCGT ACGCGGTTCT GCGCTGAAAG CGCTGGAAGG CGACGCTGAG 250
 TGGAAGCGA AAGTCGTTGA GCTGGCTGGT CACCTGGATA CTTACATTCC 300
 AGATCCAGTA CGTGCTATCG ATCTGCCGTT CCTGCTGCCA ATCGAAGACG 350
 TATTCTCAAT CTCTGGCCGT GGTACCGTTG TTACCGGTCG TGTTGAGCGC 400
 GGCATCGTGA AAGTGGGCGA CGAAGTAGAA ATCGTTGGTA TCAAAGCGAC 450
 TGCCAAGTCT ACCTGTACCG GTGTTGAAAT GTTCCGCAAA CTGCTGGACC 500
 AGGGTCAGGC AGGCGAGAAC TGTGGTGTTC TGCTGCGCGG TATCAAGCGT 550
 GAAGAGATCC AGCGTGGTCA GGTTCCTGGCT AAGCCAGGCA CCATCAAGCC 600
 50 ACACACCAAG TTCGTATCAG AAGTGACGT ACTGTCTAAA GACGAAGGCG 650
 GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCACAGTT CTAATTCCGT 700
 ACYACTGATG TGACCGGCAM CATMGAAGT CCAGAAGGCG TTGAGATGGT 750
 AATGCCAGGC GACAACATCA AAATGRCCGT TGAGCTGATC CACCCAATCG 800
 CGATGGACCA GGGTCTGCGT TTCGC 825

55

2) INFORMATION FOR SEQ ID NO: 136

60 (i) SEQUENCE CHARACTERISTICS:

82

(A) LENGTH: 762 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pasteurella multocida*
 (B) STRAIN: NCTC 10322

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136

	CACAAACACG	TGAGCACATC	CTTTTAGGTC	GCCAAGTAGG	CGTTCCTTAC	50
15	ATCATCGTAT	TCTTAAACAA	ATGCGACATG	GTGGATGATG	AAGAATTATT	100
	AGAATTAGTT	GAAATGGAAG	TGCGTGAAC	TCTTTCTCAA	TATGATTTC	150
	CAGGTGATGA	TACACCAATC	GTACGTGGTT	CAGCGTTACA	AGCGTTAAAC	200
	GGYGTAGCTG	AGTGGAAGA	GAAAATTCTT	GAGTTAGCCA	ACCACTTAGA	250
	TACTTACATT	CCAGAGCCAC	AACGTGCAAT	CGACCAACCG	TTCCTTCTTC	300
20	CGATTGAAGA	CGTGTTCCTCA	ATTTCTGGTC	GTGGTACAGT	AGTAACAGGT	350
	CGTGTGAGC	GTGGTATCAT	CCGTACAGGT	GAAGAGGTTG	AAATTGTTGG	400
	TATTAAAGCG	ACAACGAAGA	CCACAGTAAC	AGGTGTTGAG	ATGTTCCGTA	450
	AATTATTAGA	CGAAGGTCGT	GCGGGTGAGA	ACGTTGGTGC	TTTATTACGT	500
	GGTACTAARC	GTGAAGAAAT	CGAACGTGGT	CAAGTGTTAG	CGAAACCGGG	550
25	TTCAATYACG	CCACACACTG	ATTTTGAATC	AGAAGTTTAC	GTGTTATCAA	600
	AAGAAGAAGG	TGGTCGTCAT	ACACCATTCT	TCAAAGGTTA	CCGTCCACAG	650
	TTCTACTTCC	GTACAACGGA	CGTAACAGGT	ACAATCGAAT	TACCGGAAGG	700
	TGTTGAGATG	GTGATGCCTG	GTGATAACAT	CAAGATGACT	GTAAGTTTGA	750
	TTCACCCAAT	CG				762

30

2) INFORMATION FOR SEQ ID NO: 137

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Peptostreptococcus anaerobius*
 (B) STRAIN: ATCC 27337

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137

	TGGAGCTATC	TTAGTTGTAT	CAGCAGCGGA	TGGACCAATG	CCACAAACAA	50
50	GAGAACACAT	CTTATTATCA	AGACAAGTAG	GAGTACCATA	TATCGTAGTA	100
	TATTTGAATA	AAGCAGATAT	GGTAGAAGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTAAGAGAAT	TACTATCTGA	ATATGGATTG	CCAGGAGATG	200
	AAATTCCAAT	CATAACAGGA	TCATCCTTAG	GAGCATTAAA	TGGAGAACAA	250
	AAATGGATAG	ATCAAATCAT	GGCATTGATG	AAAGCCGTAG	ATGAATATAT	300
55	TCCAACACCG	GAAAGAGCAG	TAGATCAACC	ATTCTTGATG	CCAATCGAAG	350
	ACGTATTTAC	AATTACAGGA	AGAGGAACTG	TAGTAACAGG	AAGAGTTGAA	400
	AGAGGAGTTG	TAAAAGTWGG	AGAAGAAGTT	GAAATCGTAG	GAATCAAAGC	450
	GACAACAAAG	ACAACTTGTA	CYGGAGTAGA	AATGTTCCGA	AAATTATTGG	500
	ATCAAGGACA	AGCAGGAGAT	AACATCGGAG	CTTTATTTRAG	AGGAACCAAG	550
60	AAAGAAGATG	TAGAAAGAGG	ACAAGTATTG	GCAAAACCAG	GAACAATTCA	600

	TCCTCATACA	AACTTCAGTG	GAGAAGTATA	TGTATTGACA	AAAGAAGAAG	650
	GAGGAAGACA	TACTCCATTC	TTCTCAGGAT	ACAGACCACA	ATTTTACTTT	700
	AGAACCACAG	ATATTACAGG	AGCAGTAACA	TTACCAGAAG	GAGTAGAAAT	750
	GGTAATGCCR	GGAGATAATA	TCACAATGAC	AGTAGAATTG	ATTCACCCAA	800
5	TTGCAATGGA	AACAGGATTA	CGATTTGCAA	TT		832

2) INFORMATION FOR SEQ ID NO: 138

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus asaccharolyticus*
 (B) STRAIN: LSPQ 2639

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138

25	TAGTATGTTC	AGCAGCAGAY	GGTCCAATGC	CACAAACAAG	AGAACACATT	50
	CTACTAGCAA	GACAAGTTGG	TGTACCAAAG	ATAGTAGTAT	TCCTAAACAA	100
	AGAAGACCAA	GTAGACGATC	CAGAACTAAT	TGAATTAGTA	GAGATGGAAA	150
	TCAGAGACCT	ACTATCAGAA	TATGACTTCG	AYGGAGACAA	CACACCAATC	200
	GTAGTAGGAT	CAGCATTAAA	AGCCCTAGAC	GATCCAGACG	GAGAAATGGGG	250
30	AGACAAAATC	GTAAAACATA	TGGAAGMAGT	AGACGAATAC	ATCCCAACAC	300
	CAGTAAGAGA	TACAGAACAC	CCATTCTCTA	TGCCAATCGA	AGACRTATTC	350
	TCAATYACAG	GAAGAGGAAC	AGTAGCAACA	GGAAGAGTAG	AACAAGGTGT	400
	AGTAAAAGTA	GGMGACACAG	TAGAAGTAGT	AGGCTTAACA	GACGAAAGCA	450
	GACAAGTAGT	AGTAACAGGT	GTAAGAAATGT	TTAGAAAACA	ACTAGACCTA	500
35	GCAGAAGCMG	GAGACAACAT	TGGAGCCCTA	CTAAGAGGAG	TACAAAGAGA	550
	AGAAATCCAA	AGAGGACAAG	TACTAGCAGC	ACCAGGAACA	ATCAAACCAC	600
	ACACAAAATT	TGAAGCAGAA	GTATACGTAC	TAACAAAAGA	AGAAGGTGGA	650
	AGACACACAC	CATTCTTTAA	CGGATACAGA	CCACAATTCT	ACTTCAGAAC	700
	AACAGACGTA	ACAGGAGACA	TCCAACATAGC	AGACGGAGTA	GAAATGGTAA	750
40	TGCCAGGAGA	CAACTCAACA	TTTACAGTAA	CACTAATCAC	ACCAATCGCA	800
	ATGGACGAAG	GACTAAGATT	CGC			823

45 2) INFORMATION FOR SEQ ID NO: 139

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus prevotii*
 (B) STRAIN: ATCC 9321

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139

60

	CTATCATCGT	AGTATCTGCA	GCAGACGGTC	CAATGCCCAA	ACAGAGAGAA	50
	CACATCCTAC	TAGCAAGACA	AGTAGGCGTT	CCAAAAATCG	CAGTATTCCCT	100
	AAACAAAGAA	GACCAAGTAG	ACGATCCAGA	ACTAATCGAA	TTAGTAGAAA	150
	TGGAAATCAG	AGACCTACTT	TCAGAATACG	ACTTCGATGG	AGACAACGCT	200
5	CCAGTAGTAG	TAGGATCTGC	TCTTAAATCA	CTAGAAGAAG	GCGGAGAAGG	250
	CCCATGGTCA	GACAAAATCC	TTGACCTAAT	GGCACAAGTA	GACGAATACT	300
	TCGACATCCC	AGAAAAGAGAC	AACGACCAAC	CATTCCTAAT	GCCAGTAGAA	350
	GACGTAATGA	CAATCTCAGG	ACGTGGAACA	GTAGCAACAG	GAAGAGTTGA	400
	AAGAGGAACA	CTAAAAGTTG	GTGATACAGT	AGAAATCGTA	GGACTAACAG	450
10	AAGATACAAA	AGAAACAGTA	GTAACCTGGAG	TAGAAATGTT	CCACAAATCM	500
	CTAGACCAAG	CAGAATCTGG	AGATAACGTA	GGACTACTAC	TAAGAGGAGT	550
	AACAAGAGAT	CAAATCTCAA	GAGGACAAGT	ACTAGCAAAA	CCAGGWTCAG	600
	TAAACCCACA	CACAGAATTC	GAAGGTCAAG	TATACGTA	AACAAAAGAA	650
	GAAGGTGGAC	GTCACACACC	ATTCTTCAGT	GGATATAGAC	CACAATTCTT	700
15	CTTTAGAACA	ACAGACGTAA	CAGGAGACAT	CGAACTAGAA	GAAGGCGTAG	750
	AAATGGTAAT	GCCAGGAGAC	AACGCAACAT	TCAAAATCAC	ACTCCAAAAA	800
	CCAATCGCTC	TAGAAGAAGG	ACTAAGATTG	GC		832

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2) INFORMATION FOR SEQ ID NO: 140

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas asaccharolytica*

(B) STRAIN: ATCC 25260

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140

	CGGTGCTATC	ATCGTAGTTG	CTGCAACTGA	TGGTCCTATG	CCTCAGACGC	50
	GTGAGCACAT	CCTACTAGCA	CGTCAGGTCA	ACGTACCTCG	TCTAGTTGTC	100
	TTTATGAACA	AGTGCGACCT	TGTTGATGAC	GAGGAGATGC	TCGAGCTCGT	150
40	AGAGATGGAT	ATGCGTGAGC	TACTAAGCTT	CTATGACTTT	GACGGCGACA	200
	ACACTCCTGT	CATCCGTGGT	TCTGCTCTTG	GTGCTCTCAA	TGGTGAGCCT	250
	AAGTGGGTAG	AGAAGGTTAT	GGAGCTCATG	GAGGCTGTAG	ACACTTGGAT	300
	CCCACTACCT	GAGCGCGACA	TCGACAAGCC	TTTCCTAATG	CCTGTAGAGG	350
	ACGTATTCTC	TATCACAGGT	CGTGCTACTG	TCGCTACTGG	TCGTATCGAG	400
45	ACTGGTGTCT	TTAAGGTCAA	CGATGAGGTT	CAGATCATCG	GTCTAGGTGC	450
	TGAGGGTAAG	AAGAGCGTCG	TAAGTGGCGT	GGAAATGTTC	CGCAAGATCC	500
	TTGATGAGGG	TGAAGCTGGT	GATAACGTAG	GTCTCCTACT	CCGTGGTATC	550
	GACAAGGACG	AGATCAAGCG	CGGTATGGTC	CTAGCACACC	CAGGTCAGGT	600
	CAAGCCTCAC	GATCACTTCA	AGGCTGAGGT	CTATATCCTG	AAGAAGGAAG	650
50	AGGGTGGTCG	TCACACACCA	TTCCACAACA	AGTACCGTCC	TCAGTTCTAC	700
	ATCCGTACGC	TAGACGTAA	GGGCGAGATC	ACACTCCCAG	AGGGTGTAGA	750
	GATGGTTATG	CCTGGTGATA	ACGTCACCAT	CGATGTCAAG	CTCATCTCTC	800
	CAGTAGCTTG	TAGCGTAGGT	CTACGCTTCG	C		831

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2) INFORMATION FOR SEQ ID NO: 141

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 818 bases

85

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*
 (B) STRAIN: ATCC 33277

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141

	CGGTGCTATA	ATCGTTGTAG	CAGCTACAGA	CGGTCCTATG	CCTCAGACTC	50
	GCGAGCACAT	CCTTTTGGCT	CGCCAGGTAA	ACGTTCCCTCG	TCTGGTTGTT	100
15	TTCATGAACA	AATGTGACAT	GGTAGACGAT	GAAGAGATGC	TCGAGCTTGT	150
	TGAAATGGAC	ATGCGCGAAC	TCCTTTCTTT	CTACGATTTC	GATGGTGACA	200
	ATACCCCTAT	CATCCGTGGT	TCTGCTCTGG	GCGCTTTGAA	TGGAGAGCCT	250
	CAGTGGGAAG	ACAAGGTGAT	GGAGCTTATG	GAAGCTGTTG	ACAACTGGGT	300
	TCCCCTGCCT	GAGCGCGATA	TCGACAAACC	GTTCTTGATG	CCGGTTGAAG	350
20	ACGTGTTCTC	TATCACGGGT	CGTGGTACGG	TCGCTACAGG	ACGTATCGAA	400
	ACCGGTATTG	TGAAGACCGG	TGACGAAGTT	CAAATCATCG	GCCTCGGTGC	450
	AGAAGGAATG	AAGTCGGTTG	TTACGGGTGT	TGAAATGTTT	CGTAAGATTG	500
	TTGACGAAGG	TCAGGCTGGT	GACAACGTTG	GTCTCCTCCT	GCGTGGTATC	550
	GATAAGGATC	AGATCAAGCG	TGGTATGGTT	ATCTCTCACC	CGGGTAAGAT	600
25	TACTCCTCAC	AAGAGATTTA	AGGCCGAGGT	TTATATCTTG	AAGAAAGAAG	650
	AAGGTGGTCG	CCACACTCCT	TTCCACAACA	AATATCGTCC	GCAGTTCTAC	700
	ATCCGTACGC	TTGACGTGAC	CGGTGAAATC	ACTCTTCCCG	AAGGAACAGA	750
	AATGGTTATG	CCCGGTGACA	ACGTAACGAT	CACTGTAGAA	CTCATCTACC	800
	CGGTTGCATG	TAATGTAG				818

30

2) INFORMATION FOR SEQ ID NO: 142

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pragia fontium*
 (B) STRAIN: ATCC 49100

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142

	CGGCGCTATT	CTGGTTGTTG	CTGCAACTGA	TGGTCCTATG	CCTCAAATC	50
50	GTGAGCACAT	CCTGTTAGGY	CGCCAGGTTG	GCGTACCATA	CATCATTTGT	100
	TTCCTGAACA	AGTGTGACAT	GGTTGAYGAT	GAAGAGCTGT	TAGAATGGT	150
	TGAAATGGAA	GTTCTGTGAG	TTCTGTCTCA	GTACGATTTC	CCAGGTGATG	200
	ATACTCCAGT	TGTTCTGTGGT	TCTGCGCTGA	AAGCGTTRGA	AGGCGAAGCT	250
	GAGTGGGAAG	CTAAAATCAT	TGAATTGGCT	GACTCCCTGG	AYAGCTACAT	300
55	TCCACAGCCA	GAGCGTGCAA	TTGATAAGCC	GTTCTTGCTG	CCAATCGAAG	350
	ACGTTTTCTC	AATCTCTGGC	CGTGGTACAG	TAGTAACCGG	TCGTGTAGAG	400
	CGCGGTATCG	TTAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	TACTGTGAAA	ACAACCTTGA	CTGGCGTTGA	AATGTTCCGT	AARTTACTGG	500
	ATGAAGGCCG	TGCGGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTACTAAG	550
60	CGTGATGAAA	TCGAACGTGG	TCAAGTATTA	GCAAAACCAG	GTTCAATCAA	600

	CCCGCATACT	AACTTCGTAT	CAGAAGTTTA	TATCCTGAGC	AAAGATGAAG	650
	GTGGTTCGTCA	TACTCCATTC	TTCAAAGGCT	ACCGTCCACA	GTTYTACTTC	700
	CGTACAACCTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGTGATAACA	TTCAGATGAC	TGTAACCTCTG	ATTGCCCCAA	800
5	TCGCGATGGA	CGAAGGTTTA	CGCTTCGCTA			830

2) INFORMATION FOR SEQ ID NO: 143

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Prevotella melaninogenica*
 (B) STRAIN: ATCC 25845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143

25	TGGTGCTATC	TTGGTTGTAG	CTGCTACTGA	TGGTCCTATG	CCTCAGACTC	50
	GTGAGCACGT	ATTGCTCGCT	CGTCAGGTAA	ACGTACCTCG	CTTGGTTGTA	100
	TTCTTGAACA	AGTGTGATAT	GGTTGACGAT	GCTGAGATGC	TTGACCTCGT	150
	TGAGATGGAG	GTTTCGTGAGA	TCCTCGAGCA	GTACGGTTAT	GAGGAGGATA	200
	CTCCTATTAT	TCGTGGTTCT	GCACTCGGTG	CTTTGAACGG	TGTTGAGAAG	250
30	TGGGTAGACT	CTGTAATGGA	GCTCATGGAT	ACTGTTGACA	CTTGGATTGA	300
	AGAGCCAGAG	CGTGAGATTG	ACAAGCCATT	CTTGATGCCT	GTTGAGGACG	350
	TATTCTCTAT	CACAGGTCGT	GGTACTGTAG	CTACTGGTCG	TATCGAGACT	400
	GGTATCTGTA	AGGTAGGTGA	TGAGGTTTCA	TTGCTCGGTC	TCGGTGAGGA	450
	CAAGAAGTCT	GTTATCACTG	GTGTTGAGAT	GTTCCGTAAG	AACCTTCCAA	500
35	CAGGTCAGGC	TGGTGACAAC	GTAGGTCTCC	TCCTTCGTGG	TATCGATAAG	550
	GCTGAGGTTA	AGCGTGATAT	GGTTGTTGTG	CACCCAGGTG	CTATTACTCC	600
	TCACGATCAC	TTCAAGGCAT	CTATCTATGT	ATTGAAGAAG	GAAGAGGGTG	650
	GTCGTCATAC	TCCATTCGGT	AACAAGTATC	GTCCACAGTT	CTACCTCCGT	700
	ACAATGGACT	GTACAGGTGA	AATCCACCTC	CCAGAGGGCG	TTGAGATGGT	750
40	TATGCCAGGT	GACAACGTAG	AGATTGAAGT	TGTATTGATC	TATAAGGTTG	800
	CTTTGAACGA	GGGTCTTCGT	T			821

45 2) INFORMATION FOR SEQ ID NO: 144

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Prevotella oralis*
 (B) STRAIN: ATCC 33269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144

60

	TGGTGCTATT	CTTGTAAGTAG	CTGCTACTGA	CGGTCCTATG	CCTCAAACCTC	50
	GTGAACACGT	GCTTCTTGCT	CGTCAGGTGA	ACGTACCTCG	TTTGGTCGTT	100
	TTCTTGAACA	AGTGCGATAT	GGTTGACGAT	GAAGAAATGC	TTGAGCTCGT	150
	AGAAATGGAG	CTTCATGAAC	TTCTCGAGCA	GTATGAATAT	GAGGAGGATA	200
5	CTCCTATTGT	TCGTGGTTCG	GCACTTGGCG	CTCTGAATGG	AGTAGAGAAG	250
	TGGGTTGACA	GCGTGATGAA	GTTGATGGAT	ACCGTTGATG	AATGGATACA	300
	GGAACCACCG	CGTGATCTTG	ATAAGCCTTT	CTTGATGCCG	GTAGAGGATG	350
	TATTTTCTAT	TACTGGTCGT	GGAACGGTTG	TTACAGGCCG	TATTGAAACT	400
	GGTAAGGTTA	AGGTGGGCGA	TGAAGTTCAA	CTTCTTGCTC	TCGGTGAAGA	450
10	TAAGAAGTCC	GTTGTGACAG	GCGTTGAGAT	GTTCCGTAAG	ATTCTTGACG	500
	AAGGTGAAGC	TGGTGATAAT	GTAGGCTTGC	TGCTTCGTGG	TATCGATAAG	550
	ACGGAAGTAA	AGCGTGGTAT	GGTTGTCTGTA	CATCCGGGGG	CTATTACTCC	600
	TCACGATCAT	TTCAAGGCTT	CAGTTTACGT	ATTGAAGAAA	GAAGAAGGCG	650
	GTCGCCATAC	TCCGTTTGGT	AMCAAGTATC	GTCCACAGTT	CTATCTTCGT	700
15	ACCATGGACT	GTACTGGTGA	AATTACTCTT	CCGGAAGGAG	TTGAGATGGT	750
	AATGCCGGGT	GATAACGTCG	AAATTGAAGT	TAAGTTGATC	TATCCGGTAG	800
	CTTTGAACGA	GGGACTTCGT	TTCGCTA			827

20

2) INFORMATION FOR SEQ ID NO: 145

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Propionibacterium acnes*
 (B) STRAIN: ATCC 6919

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145

	CGGCGCCATC	CTCGTGGTTG	CTGCTACCGA	CGGCCCCGATG	CCTCAGACTC	50
	GCGAGCACGT	TCTGCTCGCT	CGTCAGGTGG	GCGTGCCCGC	CATCGTCGTC	100
	GCCCTCAACA	AGTGCGACAT	GGTTGACGAT	GAGGAGCTCA	TTGAGCTCGT	150
40	CGAGATGGAG	GTCCGCGAGC	TGCTGACCTC	GCAGGAGTTC	GACGGCGACA	200
	ACTGCCCTGT	CGTTCGCATC	TCCGCCTTCC	AGGCCCTCCA	GGGTGATGAG	250
	AAGTGGACCC	AGTCGATCCT	CGACCTCATG	GACGCCGTGG	ACGAGTACAT	300
	CCCGCAGCCT	GAGCGCGATC	TCGACAAGCC	CTTCCTTATG	CCGATCGAGG	350
	ACGTCTTCAC	CATCACCGGC	CGTGGCACCG	TTGTCACCGG	TCGTGTCGAG	400
45	CGCGGCGTCG	TCAAGACTGG	CGAAGAGGTC	GAGATCGTCG	GTATCCACGA	450
	GAAGACCCAG	AAGACCACCG	TTACCGGTGT	CGAGATGTTC	CGCAAGATCC	500
	TCGACGAGGG	CCGCGCTGGT	GAGAACGTCG	GCGTTCGTCT	CCGTGGCACC	550
	AAGAAGGAGG	ATGTCGTTCG	CGGCATGGTC	CTCTCCAAGC	CTGGTTCCAC	600
	CACCCCCCAC	ACCGACTTCG	AGGGCCAGGT	CTACGTCCTC	AAGAAGGATG	650
50	AGGGTGGCCG	CCACAAGCCG	TTCTTCTCCC	ACTACAGCCC	CCAGTTCTAC	700
	TTCCGTACCA	CGGACGTGAC	TGGCACTGTT	GAGCTCCCCG	AGGGCACCAG	750
	GATGGTCATG	CCTGGCGACA	ACACCGACAT	GACTGTGCAC	CTGATTACCC	800
	CGGTTGCCAT	GGAGGATCAG	CTCAAGTTCG	CTA		833

55

2) INFORMATION FOR SEQ ID NO: 146

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*
 (B) STRAIN: ATCC 35659

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146

	CACAACTCG	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCCCTTAC	50
	ATCATCGTAT	TCCTGAACAA	ATGTGACATG	GTAGATGATG	AAGAGCTGTT	100
15	AGAATTAGTT	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAA	TACGATTTCC	150
	CAGGTGATGA	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	200
	GGCGAAGCAG	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	250
	TTCTTATATC	CCAGAGCCAG	AGCGTGCAAT	TGACAAACCA	TTCCTGTTAC	300
	CAATCGAAGA	TGTATTCTCA	ATCTCAGGCC	GTGGTACAGT	AGTTACTGGT	350
20	CGTGTAGAGC	GTGGTATCAT	CAAAGTAGGT	GATGAAGTTG	AGATTGTTGG	400
	TATCAAAGAA	ACCGCCAAA	CAACTTGTA	TGGCGTTGAA	ATGTTCCGTA	450
	AATTACTTGA	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	500
	GGTACAAAAC	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CRAAACCAGG	550
	CTCAATCAAC	CCACACAACA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	600
25	AAGATGAAGG	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	650
	TTCTACTTCC	GTACAACTGA	CGTAACTGGT	ACTATCGAAT	TACCAGAAGG	700
	CGTAGAAATG	GTAATGCCAG	GCGACAACGT	GAACATGATC	GTTGA	745

30

2) INFORMATION FOR SEQ ID NO: 147

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus penneri*
 (B) STRAIN: ATCC 33519

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147

	GGAGCTATCC	TGGTTGTTGC	TGCGACAGAT	GGCCCAATGC	CACAACTCG	50
	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCCCTTAC	ATCATCGTAT	100
	TCCTGAACAA	ATGTGACATG	GTAGATGATG	AAGAGTTACT	GGAATTAGTM	150
50	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTCC	CAGGTGATGA	200
	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCAG	250
	AGTGGGAAGC	AAAATTGTT	GAATTAGCAG	AAGCACTGGA	TTCATACATC	300
	CCAGARCCAG	AGCGTGCAAT	TGACAAACCA	TTCCTGTTAC	CAATTGAAGA	350
	CGTATTCTCA	ATTTTCAGGCC	GTGGTACAGT	AGTAACAGGT	CGTGTGAGC	400
55	GTGGCGTAAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATTAAACCA	450
	ACAGCGAAAA	CAACTTGTA	TGGCGTTGAA	ATGTTCCGTA	AATTACTTGA	500
	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTTCTGCGT	GGTACTAAAC	550
	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CGAAACCAGG	TTCAATCAAC	600
	CCACACACTA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	650
60	TGGTCGTCAT	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700

GTACAACTGA	CGTAACTGGT	ACTATCGAAT	TACCAGAAGG	CGTAGAAATG	750
GTAATGCCAG	GTGACAACAT	CAACATGATC	GTTGAACTGA	TTCACCCAAT	800
CGCGATGGAC	GACGGTTTAC	GTTTCGCTA			829

5

2) INFORMATION FOR SEQ ID NO: 148

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus vulgaris*
 (B) STRAIN: ATCC 13315

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148

CGGAGCTATT	CTGGTTGTTG	CTGCGACTGA	TGGCCCAATG	CCACAAACTC	50
GTGAGCACAT	CCTGTTAGGT	CGCCAGGTTG	GTGTACCTTA	CATCATCGTA	100
TTCCTGAACA	AATGTGACAT	GGTTGATGAT	GAAGAACTGC	TGGAATTAGT	150
AGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTT	CCAGGTGATG	200
ACACTCCAGT	AATCCGTGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAAGCT	250
GAGTGGGAAG	CAAAAATTGT	TGAATTAGCA	GAAGCACTGG	ATTCTTACAT	300
CCCAGAACCA	GAGCGTGCAA	TTGACAAACC	ATTCTTGCTG	CCTATCGAAG	350
ACGTATTCTC	AATCTCTGGT	CGTGGTACAG	TAGTAACAGG	CCGTGTAGAG	400
CGTGGTGTG	TTAAAGTTGG	TGAAGAAGTT	GAGATTGTTG	GTATTAAAGA	450
CACAGTTAAA	ACAACCTTGT	CTGGCGTTGA	AATGTTCCGT	AAATTACTTG	500
ACGAAGGTCG	TGCAGGTGAG	AACGTAGGTG	TTCTTCTGCG	TGGTACTAAA	550
CGTGAAGAAA	TCGAACGTGG	ACAAGTACTG	GCTAAACCAG	GTTCAATCAA	600
GCCACACACT	AAATTCGAAT	CAGAAGTTTA	TATCCTGAGC	AAAGATGAAG	650
GTGGTCGTCA	CACTCCATTC	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
CGTACAACCTG	ACGTAACTGG	TACTATCGAA	TTACCAGAAG	GCGTAGAAAT	750
GGTAATGCCA	GGTGACAACA	TCAACATGAT	CGTTGAACTG	ATTCACCCTA	800
TCGCGTAGGA	CGACGGTTTA	CGTT			824

40

2) INFORMATION FOR SEQ ID NO: 149

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 745 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Providencia alcalifaciens*
 (B) STRAIN: ATCC 9886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149

CACAAACTCG	TGAGCACATC	CTGTTAGGTC	GCCAAGTAGG	TGTTTCCTTAC	50
ATCATCGTTT	TCCTGAACAA	ATGTGACATG	GTAGACGACG	AAGAACTGTT	100

90